

From:

Riggins, Patrick S.

Sent:

Monday, February 07, 2005 8:35 AM

To:

STIC-Biotech/ChemLib

Subject:

seq search

This is in regard to case #10006265

Please search SEQ ID NOs, 2, 4, and 17(protein) against the commercial <u>nucleotide</u> databases in both a standard search and a standard oligomer search. The following information may be helpful in the search. I previously requested an alignment of these sequences. The results were as follows: SEQ ID NOs 2 and 17 are identical from 1-642. SEQ ID NO 2 and 17 are identical with SEQ ID NO 4 from 1-238. If this is in any way unclear, please call and I'll be happy to clarify.

The claims of interest are appended below. If you identify any other necessary searches based on these claims I would appreciate they be performed also. I'm fairly confident I have requested all that is necessary though. Incidentally, SEQ ID NOs 1, 3, and 16 encode SEQ ID NOs 2, 4, and 17, respectively.

1. An isolated nucleic acid of any one of (a) to (d) below:

(a) a nucleic acid encoding a protein comprising the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17,

(b) a nucleic acid comprising a coding region in the nucleotide sequence of any

one of SEQ ID NOs:1, 3 or 16,

(c) a nucleic acid encoding a protein that comprises the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17, in which one or more amino acids are replaced, deleted, inserted and/or added and that is functionally equivalent to the protein comprising the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17, and

(d) a nucleic acid that hybridizes under stringent conditions with the nucleic acid comprising the nucleotide sequence of any one of SEQ ID NOs:1, 3 or 16, and that encodes a protein functionally equivalent to the protein comprising the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17.

2. An isolated nucleic acid encoding the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17 or a fragment thereof.

Thank you, Pat Riggins

Patrick Riggins Examiner Art Unit 1636 REM 3A64 571-272-6102 (STIC)

STAFF USE ONLY	
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-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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MASATSUGU MAEDA, NORIKO YAGUCHI	
PR 02-JUN-1999 JP 99P 155797,30-JUL-1999 JP 99P 217797 PI	
01-JUN-2000 WO 2000JP003556	
PN WO 0075314-A/1	
OS Homo sapiens (human)	MMENT
MAEDA, NORIKO YAGUCHI	
CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU	
Patent: WO 0075314-A 1 14-DEC-2000;	JOURNAL
Novel hemopoietin receptor protein, NR10	TITLE
Maeda, M. and Yaguchi, N.	AUTHORS
(bases 1 to 2969)	FERENCE
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
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Novel hemopoietin receptor protein, NR10.	FINITION
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AL Patent: WO 0075314-A 14 14-DEC-2000;
CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU MARDA, NORIKO YAGUCHI
OS Homo sapiens (human)
PN WO 0075314-A/14
PD 14-DEC-2000
PF 01-UN-2000 WO 2000JP003556
PF 01-UN-1999 JP 99P 155797,30-JUL-1999 JP 99P 217797 PI
MASATSUGU MAEDA,NORIKO YAGUCHI
PC CI2NI5/12,C12N5/10,C07K14/715,C07K16/28,C12P21/02,G01N33/53,
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PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys
                                                     GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGly
                                                                                                        LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Patent: WO 0200721-A 53 03-JAN-2002;
ZymoGenetics, Inc. (US)
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/db xref="taxon:9606"
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                                                                                                 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn
                                                                                                                                                          CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal
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                                                     GlnGluLysGlnPheArgArgGlyLysGluTrpAsp 652
                                                                                                                                                     LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
                                                                                                                                                                                                                                                                                                       TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
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                                                                                                                                                                                                                              ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
                                                                                                                                                                                                                                                                                                                                                            AAATTGACTCATCTGTGTTGGCCCACCGTTCCCAACCCTGCTGAAAGTAGTATAGCCACA
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
                                                       Query Match:
DB:
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2 (bases 1 to 2903)
2 (bases 1 to 2903)
2 (bases 1 to 2903)
Dillon, S. R., Sprecher, C., Hammond, A., Rosenfeld-Franklin, M.,
Presnell, S. R., Haugen, H., Bilsborough, J., Maurer, M., Harder, B.,
Johnston, J., Bort, S., Mudri, S., Kuijper, J., Bukowski, T., Shea, P.,
Johnston, J., Bort, S., Mudri, S., Kuijper, J., LeCeil, C., Waggie, K.,
Dong, D., Dasovich, M., Lockwood, L., Levin, S., LeCeil, C., Waggie, K.,
Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parrish-Novak, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2903 bp mRNA linear PRI 10-JUL-2004
Homo sapiens interleukin 31RA splice variant x4 (IL31RA) mRNA,
complete cds, alternatively spliced.
AV499342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics,
Eastlake Avenue East, Seattle, WA 98102, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin 31, a cytokine produced by dermatitis in mice Nat. Immunol. 5 (7), 752-760 (2004)
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1 (bases 1 to 2903)

Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J.,

Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,

Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J.L.,

Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,

Lockwood,L., Levin,S.D., LeCiel,C., Waggie,K., Day,H., Topouzis,S.

Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                            / Jones = "Class I cytokine receptor; huzcytor17x4;
alternatively spliced"
//codon_start=1
//codon_start=1
//product="interleukin 31RA splice variant x4"
//product="i
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497. .2485
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1, .2903
GNVLQEIFTDEARTGQENNLGGEKNGTRILSSCPTSI"
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/db_xref="taxon:9606"
/chromosome="5"
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|mol_type="mRNA"
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Alignment Scores: Pred. No.: Percent Similarity: Best Local Similarity: 3.22e-300 3451.00 99.85% 99.69% 99.05% Length: Matches: Conservative: Mismatches: Indels:

US-10-006-265-2 (1-652) x AY499342 (1-2903) 뭐 δ B S 밁 S 용 ঠ 밁 ঠ 문 5 뭐 Ś 밁 á В S 망 ঠ , <u>B</u> र् 日 ð 밁 5 밁 Ś 당 S 밁 S 밁 5

361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380	57 CTTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCCAGCTATTCAAGAAAAATCATTTCAG 151 41 CysileGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360	-% <u>5</u> _F	1 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300 	ArgGeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsm 2 	CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 2 	1 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240 	l LeuThrGlyLeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGlu 2	81 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 2	161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180 	141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160 	LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 14	IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle	81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 10	1 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80	41 IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 6 	TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40 	1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
AUTHORS Sprecher, C.A., Prance and Maurer, M.F.		AX365193 LOCUS AX365193 LOCUS AX365193 ACCESSION AX365193 VERSION AX365193.1 GI:10	641 GlnGlu	Qy 621 LeuValValAsnPhs	Qy 601 ThrGluAspArgIIs 	Qy 581 TrpHisGlyAspAsp 	ω— E	Oy 541 GlyGlyGlyLeuLeu	Qy 521 IleAspPheLysThi 	501 ThrSer 1997 ACCTCT	481 PheSer 1937 TTCTCC	Qy 461 GluArgLy8Gly116 	Qy 441 LysValGluAsnIle 	Qy 421 GluProTyrSerIle 	Qy 401 LeuLy8ProPheTr; 	Qy 381 ThrThrLeuSerTry	Db 1577 TCTGCTCTAGACGTC
Presnell,S.R., Gao,Z., Whitmore,T.E., Kuijper,J.L.	an) a; Chordata; Craniata; Vertebrata; Euteleostomi; a; Primates; Catarrhini; Hominidae; Homo.	2529 bp DNA linear PAT 15-FEB-2002 from Patent WO0200721.	LysGlnPheArgArgGlyLysGluTrpAsp 652 	ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640 	AspArgIleLeuLysProCysSerThrProSerAspLysLeuVallleAspLys 620 	GlyaspaspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600 	ThrHisLeuCysTrpProThrValProAsnProAlaCluSerSerIleAlaThr 580 					LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGly 480 	GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460 	TyrSerIleGlmAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440 	ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420 	LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400 	

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	AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer	ValLysBroValLeuGlyIleLysArgMetIleGlnIleGluTxpIleLysProGluLeu : [HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg	IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer	ThrashSerSerThrSerGluAshArgAlaSerCysSerPhePheLeuProArgIleThr	eGlyGluLysHisAspAsnCysThr TGGAGAAAACATGATAATTGTACA	Cy8ValTyrTyrTyrArgLy8AsnLeuThrCy8ThrTrpSerProGlyLy8GluThrSer 6	LeuProSerLeuCysLysDheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 4	LeuSerProGlnProSerCy8ValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 2 	98.77% Indels: 6 Gaps:) x AX365193 (1-2529)	Alignment Scores: 2.12e-299 Length: 2529 Score: 3441.00 Matches: 648 Percent Similarity: 99.85% Conservative: Best Local Similarity: 99.69% Mismatches:		CYNIS VY PMLHIKYGEP YSIQAY AKEGYPSEGPETKVENIG VKTVTITINKEI PKSEK GIICNYTIF YQAEGGKGFSKTVNSSILQYGLESLKRYSY I VQYMASTSAGGTNGTSI NFKTLSFSVFEI ILITSLIGGGLLILI ILTVAYGLKKPNKLTHLCWPTVENPAESSIA TWHGDDFKDKLNLKESDDSVNTEDRILKFCSTFSDKLVLIKLVVNFGNVLQEI FTDEA	RFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVIALRCAVKESKFWSDWSQEK MGMTEBEAPCGLELWRVLKPAEADGRRPVRLLWKKARGAPVLEKTLGYNIWYYPESNT NLTETWNTTNQQLELHLGGESFWYSMISYNSLGKESPVATLRIPALQEKSFQCIEVNQA CVAEDOLANKAGSSALANTWATEWEDDINTGESPTTISWESWSCALWWTGODYL XEWS	/db_xref="G1:18696950" /translation="MMMTWALMILDSLCKFSLAALPAKPENISCYYYYRKNLTCTWSP /translation="MMMTWALMILDSLCKFSLAALPAKPENISCYYYYRKNLTCTWSP GKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRASCSFFLPRITIPDNYTIEVEAEN GDGVIKSHMTWARLENLAKTEPPKIFNKFSTAKANIOTEWIKPELAFVSSDLKYTL	<pre>/note="unnamed protein product" /codon_start=1 /protein_id="CAD23790.1"</pre>	signed D	Location/Qualifiers 12529 /organism="Homo saniens"	Tocation/Onalifiers
543	Qy 523 PhotysThrteuSerPheSerValPheGluIleIIleIeuIleThrSerteuIleGlyGly 182		1569	1509	1449	Qy 423 Db 1389	62 TOP TOP TO THE PROPERTY OF	1269	363 1209			Qy 303 GluLeuHisieuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly	Qy 283 Db 969	QY 263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp SNT	Qy 243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu MSP		Db 729 GGGCTGCAGCCTTTTACAGAATATGTCATAGCTCTGCGATGTGCGGTCAAGGAGT	Qy 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys	THE TOTAL TO

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1 (bases 1 to 2529)

Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J.,

Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,

Harder,B., Johnston,J., Bort,S., Mudir,S., Kuljper,J.L.,

Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,

Lockwood,L., Levin,S.D., LeCiel,C., Waggie,K., Day,H., Topouzis,S.,

Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
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AY499339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatitis in mice
Nat. Immunol. 5 (7), 752-760 (2004)
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/gene="II31RA"
/note="class I cytokine receptor; huzcytor17x1;
alternatively spliced"
/codon_start=1
/product="interleukin 31RA splice variant x1"
/protein_id="AAS86444.1"
                                                                                                                                                                                                                     /gene="IL31RA"
162. .2111
                                                                                                                                                                                                                                                                                                                       map="5q11"
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chromosome="5"
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/db_xref="GI:46276457"
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Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: DB:	2.12e-299 Length: 2529 3441.00 Matches: 648 iilarity: 99.85% Conservative: 1 similarity: 99.69% Mismatches: 1 98.77% Indels: 1 9 Gaps: 0
US-10-006-2	.65-2 (1-652) x AY499339 (1-2529)
Qy	3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
Db 12	9 CTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGTGATGTGGACCTGGGCACTGTGGGA
Ş	23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
Db 1	89 CTCCCCTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAAACATTTC
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Db 2	249 TGTGTCTACTATAGGAAAAATTTAACCTGCACTTGGAGGTCCAGGAAAGGAAACCAGT 308
Ş	63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 82
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0у 1	.03 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
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Db 5	49
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Db 7	89 TTCTGGAGTGACTGGAGCCAAGAAAAAATGGGGAATGACTGAGGAAGAAGCTCCATGTGGC 848

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                                                                                                           ACTCATCTGTGTTGGCCCACCGTTCCCCAACCCTGCTGAAAGTAGTATAGCCACACTGGCAT
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 4315)

RS Maeda, M., Yaguchi, N. and Hasegawa, M.

RN10 splicing varinats

AL Patent: WO 02077230-A 1 03-OCT-2002;
CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,
MASAKAZU HASEGAWA

OS HOMO sapiens (human)
PN WO 02077230-A/1
PD 03-OCT-2002
PF 22-MAR-2002 WO 2002JP002769
PR 26-MAR-2001 JP 01P 087298
PI MASATSUGU MAEDA, NORIKO YAGUCHI, MASATSUGU HASEGAWA PC
C12N15/12, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
CC NR10 splicing varinats
FH Key

LOCation/Qualifiers

CT C12F1/Orelifice.
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BD178870.1 GI:30016137
WO 02077230-A/1.
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NR10 splicing varinats.
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                                                 TGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAAACCAGT
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/db_xref="taxon:9606"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, I
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                    Cosman,D.J., Mosley,B.A., Bird,T.A., lematopoietin receptors hpr1 and hpr2 Patent: WO 0229060-A 5 11-APR-2002; Immunex CorporatioN (US)
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1 (bases 1 to 2393)

Dillon, S.R., Sprecher, C., Hammond, A., Bilsborough, J.,
Rosenfeld-Franklin, M., Presnell, S.R., Haugen, H.S., Maurer, M.,
Harder, B., Johnston, J., Bort, S., Mudri, S., Kuijper, J.L.,
Bukowski, T., Shea, P., Dong, D.L., Dasovich, M., Grant, F.J.,
Lockwood, L., Levin, S.D., LeCiel, C., Waggie, K., Day, H., Topouzis, S.,
Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parrish-Novak, J. and
Gross, J.A.
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Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics,
Eastlake Avenue East, Seattle, WA 98102, USA
Location/Qualifiers
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Presnell,S.R., Haugen,H., Bilsborough,J., Maurer,M., Harder,B.,
Johnston,J., Bort,S., Mudri,S., Kuijper,J., Bukowski,T., Shea,P.,
Dong,D., Dasovich,M., Lockwood,L., Levin,S., LeCeil,C., Waggie,K.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
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Nat. Immunol. 5 (7), 752-760 (2004)
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                                                                                                                           Sprecher, C.A., and Maurer, M.F. Cytokine recept
                                                                                    Cytokine receptor zcytor17
Patent: WO 0200721-A 1 03-JAN-2002;
ZymoGenetics, Inc. (US)
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Sequence 1 from Patent WO0200721.
AX365149
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Location/Qualifiers
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Eutheria;
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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                                           GGCCTTCTTATTCTCATTATCCTGACAGTGGCATATGGTCTCAAAAAACCCCAACAAATTG
                                                      GlyLeuLeuIleLeuIleLleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu
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Hematopoietin receptors hpr1 and hpr2
Patent: WO 0229060-A 3 1-APR-2002;
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                                                               CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg
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            GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGly 480
                                                                                                                    GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
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                                                                 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer
                                                                                                      GAGCCATATTCCATCCAGGCTTATGCCAAAGAAGGCGTTCCATCAGAAGGTCCTGAGACC
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Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 2952)
RS Maeda, M., Yagyuchi, N. and Hasegawa, M.
NR10 splicing varinats
AL Patent: WO 02077230-A 3 03-OCT-2002;
CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,
MASAKAZU HASEGAWA
OS HOMO 8apiens (human)
PN WO 02077230-A/3
PD 03-OCT-2002
PF 26-MAR-2002 WO 2002JP002769
PF 26-MAR-2001 JP 01P 087298
PR 26-MAR-2000 WO 2002JP002769
PR 26-M
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NR10 splicing varinats.

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BD178872.1 GI:30016139

MO 02077230-A/3.
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Location/Qualifiers
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/db_xref="taxon:9606"
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Qy 283 TYTTYTPTOGIUSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302	Qy 243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262	Qy 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222	CTGATTTAAAATACACACTTCGATTCAG SnPheAlaLysAsnArgLysAspLysAs 	Qy 143 ValLysProValLeuGlyIleLysArgMetIleGlnIIeGluTxpIleLysProGluLeu 162	Db 370 ATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATTAAATCT 429 Qy 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142	83 ThrashserserThrserGluashargAlaserCysserPhePheLeubroArglieThr	63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr	43 CysvalTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62	Db 70 CTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTGTGGATG 129 Qy 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42	US-10-006-265-2 (1-652) X BU1/88/2 (1-2952) QY	98.59% Indels: 6 Gaps:	Pred. No.: 9.08e-299 Length: 2952 Score: 3435.00 Matches: 647 Percent Similarity: 99.85% Conservative: 1
Oy 643 LyeGlnbheArgArgGlyLyeGlTTrp 651		1750 583 1810	Db 1630 TTCAAGACATTGTCATTCAGTGTCTTTGAGATTATCCTCATAACTTCTCTGATTGGTGGA 1689 Qy 543 GlyLeuLeuIleLeuIleIleLeuThrValalaTyrGlyLeuLysLysProAsnLysLeu 562	503 TyrllevalGinvalmecAlaAsminrSeralaGyGlynnrAsmolyInrSerileAsm 5/2	483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 5	Db 1390 GAGAACATTGGCGTGAAAGGGTCACGATCACGAGAGAGAG	Qy 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal 442	Qy 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro 422	383 1210	Qy 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382	Qy 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAla 362	Oy 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342

B		Query Matc DB: US-10-006- Qy Db Qy	FEATURES BOUICE ORIGIN Alignment S Pred. No.: Score: Percent Sim Best Local:	VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT
103 11eProAspAsnTyrThrI1eGluValGluAlaGluAsnGlyAspGlyValI1eLysSer 122	43 CysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 6	98.59% Indels: 6 Gaps: 6 Gaps:) x BD178871 (1-5271)) x BD178871 (1-5271)	CC C12P21/02,G01N33/15,G01N33/50,G01N33/53 CC NR10 splicing varinats FH Key Varinats Location/Qualifiers FEATURES FOR CDS Location/Qualifiers 1.5271 Location/Qualifiers 67) FORGIN ORIGIN ORIGIN Alignment Scores: Pred. No.: Percent Similarity: 99.85% Best Local Similarity: 99.69% Matches: 1 Magnatches: 1 Magnatches: 1 Magnatches: 1 Magnatches: 1 Magnatches: 1	BD178871.1 GI:30016138 WO 02077230-A/2. Homo sapiens (human) NHomo sapiens (human) SM Homo sapiens (human) SM Homo sapiens (human) SM Homo sapiens (hordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5271) SM (hases 2 to 5711) SM (hases
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1450 AAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGAGGAGGAAAAGGATTCTCC 1509 483 LYBThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502	403 FYROFREIT PCYSTYFASHILESET WITTYFFFOMELLEULISASDYSVALUTYGILFTO 4.22 1270 CCTTTCTGGTGCTATAACATCTCTGTGTATCCAATGTTGCATGACAAAGTTGGCGAGCCA 1329 423 TYTSETILEGINALATYTALALYSGIUGLYVALPROSETGIUGLYPROGIUTHTLYSVAL 442 1330 TATTCCATCCAGGCTTATGCCAAAGAAGGCGTTCCATCAGAAGGTCCTAAGACCAAGGTG 1389 443 GluhsnileglyvallysThrvalThrileThrTrpLysGluIleProLysSerGluhrg 462	3 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLySTrpGlnSerSerAla	263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282	163 AlaProvalSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182

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Percent Similarity:
Best Local Similarity:
Query Match:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3072)

8 Maeda, M., Yaguchi, N. and Hasegawa, M.

NR10 splicing varinats

CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,
MASAKAZU HASEGAWA

OS Homo sapiens (human)
PN WO 02077230-A/4
PD 03-OCT-2002
PF 22-MAR-2002 WO 2002JP002769
PR 26-MAR-2001 JP 01P 087298
PR MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
C12N15/12,C07K14/715,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/22,G01N33/15,G01N33/50,G01N33/53
FH Key
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(7), (1887).
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                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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93.90%
97.73%
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            (1-3072)
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                                  GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAla
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                                                                             LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle
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AF486620.1 G:
                                                                                                                             LysGlnPheArgArgGlyLysGluTrp 651
                                                                                                                                                                         GTGAACTTTGGGAATGTTCTGCAAGAATTTTCACAGATGAAGCCAGAACGGGTCAGGA-
                                                                                                                                                                                         ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
                                                                                                                                                                                                                                                         AspArgILeLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyAspAspPheLys------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTTCCTGGGAATCTGTGTCTCAGGCCACGAACTGGACGATCCAGCAAGATAAATTAAAA
                                                                                                                                                                                                                                       GACAGGATCTTAAAAACCATGTTCCACCCCCAGTGACAAGTTGGTGATTGACAAGTTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTCATCTGTGTTGGCCCACCGTTCCCAACCCTGCTGAAAGTAGTATAGCCACATGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCTTCTTATTCTCATTATCCTGACAGTGGCATATGGTCTCAAAAAACCCAACAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAGACATTGTCATTCAGTGTCTTTGAGATTATCCTCATAACTTCTCTGATTGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ly8GlyI1eI1eCy8AsnTyrThrI1ePheTyrGlnAlaGluGlyGlyLy8glyPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGACAGTCAATTCCAGCATCTTGCAGTACGGCCTGGAGTCCCTGAAACGAAAGACCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGGAAAAGGATTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTTTCTGGTGCTATAACATCTCTGTGTATCCAATGTTGCATGACAAAGTTGGCGAGCCA
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    GI:20563276
                              gp130-like monocyte receptor mRNA, complete cds.
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                                181
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CysSerPhePheLeuProArgIleThrIleProAspAsnTyrThrIleGluValGluAla
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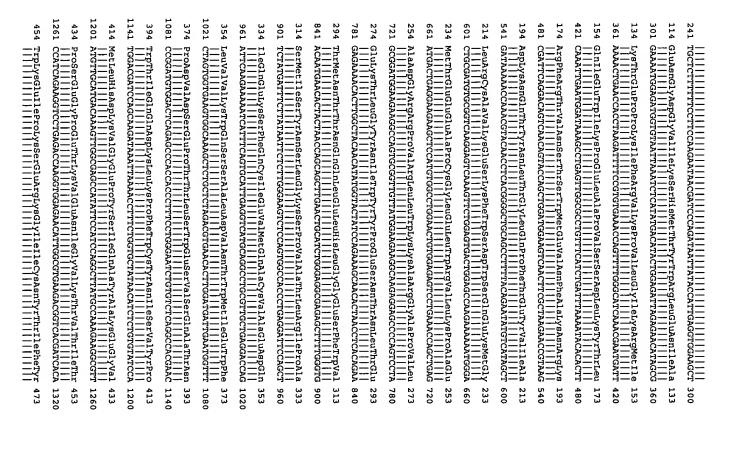
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                              34 LeuProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCys
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Ghilardi, N., Li, J., H
Sauvage, F.J.
Direct Submission
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2199)
Ghilardi,N., Li,J., Hongo,J.A., Yi,S., Gurney,A. and de
Sauvage,F.J.
A novel type I cytokine receptor is expressed on monocytes, signal proliferation, and activates STAT-3 and STAT-5
J. Biol. Chem. 277 (19), 16831-16836 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-FEB-2002) Molecular South San Francisco, CA 94080, USA Location/Qualifiers
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  TTTGGAGAAAAACATGATAATTGTACAACCAATAGTTCTACAAGTGAAAATCGTGCTTCG
                                PheGlyGluLysHisAspAsnCysThrThrAsnSerSerThrSerGluAsnArgAlaSer
                                                                                                                                                   ThrTrpSerProGlyLysGluThrSerTyrThrGlnTyrThrValLysArgThrTyrAla
                                                                                                                                                                                                                                   CTGCCAGCTAAGCCTGAGAACATTTCCT
                                                                                                                                                                                                                                                                                                                                              ATGATGTGGACCTGGGCACTGTGGATGCTCCCTTCACTCTGCAAATTCAGCCTGGCAGCT
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MGMTEBEBAPCGLELMRVLKFAEADGRRPVRLLWKKARGAPULEKTLGYNIWYYPESNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKEQLLFSGQSLVPDHLCEEGAPNPYLKNSVTAREFLVSEKLPEHTKGEV"
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                                                                                                             ICCAGGAAAGGAAACCAGTTATACCCAGTACACAGTTAAGAGAACTTACGCT
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	ThrAspGluAlaArgThrGlyGlnGluLysGlnPheArgArgGlyLysGluTrp 651	634	Ŋ.
1860	GACAAGTTGGTGATTGACAAGTTGGTGGTGAACTTTGGGAATGTTCTGCAAGAAATTTTC	1801	Дb
633	AspLysLeuVallleAspLysLeuValValAsnPheGlyAsnValLeuGlnGluIlePhe (614	Ş
1800	GAGTCTGATGACTCTGTGAACACAGAAGACAGGATCTTAAAACCATGTTCCACCCCCAGT	1741	뮍
613	GluSerAspAspSerValAsnThrGluAspArgIleLeuLysProCysSerThrProSer(594	8
1740	GCTGAAAGTAGTATAGCCACATGGCATGGAGATGATTTCAAGGATAAGCTAAACCTGAAG	1681	망
593	AlaGluSerSerIleAlaThrTrpHisGlyAspAspPheLysAspLysLeuAsnLeuLys :	574	Ş
1680	TATGGTCTCAAAAAAACCCAACAAATTGACTCATCTGTGTTGGCCCACCGTTCCCAACCCT	1621	ఠ
573	TyrGlyLeuLysLysProAsnLysLeuThrHisLeuCysTrpProThrValProAsnPro :	554	8
1620	ATCCTCATAACTTCTCTGATTGGTGGAGGCCTTCTTATTCTCATTATCCTGACAGTGGCA	1561	В
553	IleLeuIleThrSerLeuIleGlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAla :	534	8
1560	GGGGGAACCAACGGGACCAGCATAAATTTCAAGACATTGTCATTCAGTGTCTTTGAGATT	1501	망
533	GlyGlyThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSerValPheGluIle !	514	Ş
1500	CAGTGCT	1441	망
513	LeuGluSerLeuLysArgLysThrSerTyrIleValGlnValMetAlaAsnThrSerAla :	494	Ş
1440	CAAGCTGAAGGTGGAAAAGGATTCTCCAAGACAGTCAATTCCAGCATCTTGCAGTACGGC	1381	ఠ
493	GlnAlaGluGlyGlyLysGlyPheSerLysThrValAsnSerSerTleLeuGlnTyrGly	474	8
1380	TGGAAAGAGATTCCCAAGAGTGAGAGAAAGGGGATCATCTGCAACTACACCATCTTTTAC	1321	рb

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Search completed: February 23, 2005, 15:24:08 Job time: 8310.85 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    Score
    3484
3451
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Match
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1: geneseqn1980s:*
2: geneseqn1990s:*
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30-JUL-1999;
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Yaguchi N;
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Percent Similarity:
                                                                                                                                         The present sequence encodes a human haemopoietin receptor protein (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haematopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the identification of substances for the treatment and prevention of immune and haematopoietic discovers including autoimmune diseases and allergies such as metal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10; immunoregulation; haematopoietic cell regulation; transmemb immune disorder; haematopoietic disorder; autoimmune diseas metal allergy; pollen allergy; ss.
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P-PSDB; AAB51244.
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IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu

616

ATGAAGCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTG

497 21

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                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                      US-10-006-265-2 (1-652) x ABA93808 (1-2903)
                                                                                                                                                                                                    Alignment
                                                                                                                                                                                                                                                                                     zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 cantirheumatic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders. Agonists or anti-cytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducting cytocoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. zheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA33767 to ABA33363 and ABB05730 to ABB05745 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polynucleotide useful for treating and spleenic, blood or bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-090519/12.
P-PSDB; ABB05741.
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29-JUN-2000; 2000US-0214955P.
08-FEB-2001; 2001US-0267963P.
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                                                                                                                                                                                                                                      Sequence 2903
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                                                                                                                                                                                                                                                                        exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a cytokine receptor designated zcytor17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 199-203; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                        664 G;
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Matches:
Conservative:
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ss; gene; human; zcytor17; antiinflammatory; dermatological; immunosuppressive; antimitorobial; vaccine; inflammatory disease; inflammatory bowel disease; ulcerative colitis; Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia; septicaemia; toxic shock syndrome; infectious disease.

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Location/Qualifiers /product= "zcytor17" /*tag=

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New zcytor17 ligand polypeptides, useful for treating inflammatory diseases, such as inflammatory bowel disease, ulcerative colitis,
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25-APR-2002; 2002US-0375323P
19-DEC-2002; 2002US-0435315P
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                                                                                                               AAGGTGGAGAACATTGGCGTGAAGACGGTCACGATCACATGGAAAGAGATTCCCCAAGAGT
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14-JUN-2002;
19-DEC-2002;
                                                                                                                                                                                                                                                                                       antibacterial; immunosuppressive; cell proliferation inhibitor; immune response inhibitor; inflammatory response inhibitor; multimeric cytokine receptor; heterodimeric cytokine receptor; cancer; cytokine-binding domain; class I cytokine receptor; haematopoietic cell; zcytor17lig-induced proliferation; zcytor17lig-induced differentiation; hematopoietic progenitor cell; zcytor17lig-induced inflammation; inflammatory disease; inflammatory bowel disease; ulcerative collits; crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia; septicaemia; toxic shock syndrome; zcytor17; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic
                                                    (SPRE/)
(GAOZ/)
(KUIJ/)
(DASO/)
(GRAN/)
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  (HAMM/)
                            (PRES/)
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DASOVICH M M.
GRANT F J.
PRESNELL S R.
WHITMORE T E.
HAMMOND A K.
NOVAK J E.
                                                                               GAO Z.
KUIJPER J L.
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2002US-0389108P.
2002US-0435361P.
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WPI; 2003-876545/81.
P-PSDB; ADL26570.
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Presnell SR,
                                                                                                                                                 (GROS/) GRŎSS J A.
(DILL/) DILLON S R
                                                                                                                                       Gao Z, K
Whitmore
                                                                                                                                      Kuijper JL, Dasovich MM, Gı
e TE, Hammond AK, Novak JE,
                                                                                                                                           Grant FJ;
                                                                                                                                       Gross JA,
                                                                                                                                       Dillon
                                                                                                                                       SR
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Novel multimeric or heterodimeric cytokine receptors useful for treating chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, acute inflammatory disease such as endotoxemia,

Example 3; SEQ ID NO 4; 205pp; English

The invention describes an isolated multimeric or heterodimeric cytokine receptor (I) having at least one polypeptide having 90 percent sequence (C identity with a 732 (S1) or 649 (S2) amino acid sequence given in C specification, and where (I) binds a ligand comprising a 164 (S3) amino C acid sequence, given in specification, or at least one polypeptide (C comprising an antibody to (I) and a cytokine-binding domain of a class (C in cytokine receptor. A composition (C1) comprising (I) and a cytokine-binding domain of a class (C in cytokine reducing haematopoietic cells and hematopotetic progenitor cells in a mammal; inhibiting zcytor171ig-induced proliferation or differentiation (C inflammatory disease in which zcytor17lig plays a role. The disease is a crytorior17lig-induced inflammatory bowel disease is a crytorior inflammatory disease such as inflammatory bowel disease is a crytonic inflammatory disease such as inflammatory bowel disease is a crytorior response in a mammal exposed to an antigen or pathogen. An immune response in a mammal exposed to an antigen or pathogen. An confidential or inflammatory response inhibiting composition is useful for suppressing an confidential binds to (I) is useful for detecting the presence of a confidential binds to (I) is useful for detecting the presence of a confidential confidential cytokine receptor in a biological sample.

This sequence encodes a human zcytor17 cytokine receptor.

Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other

DB:	Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
11	99.05%	99.69%	99.85%	3451.00	6.92e-316	
Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
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US-10-006-265-2 (1-652) x ADL26569 (1-2903)

Ş	1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20	
망	497 ATGAAGCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGGACTG 556	o,
Ş	21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40	
망	557 TGGATGCTCCCTTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAAC 616	u
γQ	41 IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60	
B	617 ATTTCCTGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAA 676	u
Ş	61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80	
ф	677 ACCAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAAT 736	U1
β	81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100	J
망	737 TGTACAACCAATAGTTCTACAAGTGAAAATCGTGCTTCGTGCTCTTTTTTTCCTTCC	٠,

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SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro
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                                                      GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr
                                                                                                                        LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly
                                                                                                                                                                             ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys
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                                                                                                                                                                                                                                  SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro
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                                                                                                                                             Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory; antiiviral; antiirheumatic; antiarthritic; cytostatic; muscular; lymphoid; immune; inflammatory; spleenic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
Sprecher CA,
Maurer MF;
                                          26-JUN-2000; 2000US-0214282P
29-JUN-2000; 2000US-0214955P
08-FEB-2001; 2001US-0267963P
                                                                                                                                                                                                          Human zcytor17
                                                                                                                                                                                                                           01-MAY-2002
                                                                            26-JUN-2001; 2001WO-US020484
                                                                                                              WO200200721-A2
                          (ZYMO ) ZYMOGENETICS INC.
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                               2003-876545/81.
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Novel multimeric or heterodimeric cytokine receptors useful for treating chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, acute inflammatory disease such as endotoxemia,

Disclosure; SEQ ID NO 108; 205pp; English.

Creceptor (II) having at least one polypeptide having 90 percent sequence condensity with a 732 (S1) or 649 (S2) amino acid sequence given in Specification, and where (I) binds a ligand comprising a 164 (S3) amino coid sequence, given in specification, or at least one polypeptide comprising residue 20-227 of (S1). (I) is useful for killing cancer cells and producing an antibody to (I) and a cytokine-binding domain of a class I cytokine receptor. A composition (C1) comprising (I) and a cytokine-binding domain of a class I cytokine receptor and a vehicle is useful for: reducing hematopoietic cells and hematopoietic progenitor cells in a mammal; inhibiting zcytor1711g-induced proliferation or differentiation or differentiation of inflammatory disease in which zcytor1711g plays a role. The disease is a cute inflammatory bowel disease is a cute inflammatory disease such as inflammatory disease such as inflammatory disease. A copic dermatitis, eczema and confidential control of inflammatory composition is useful for inhibiting an inflammatory response inhibiting composition is useful for inhibiting an inflammatory response inhibiting composition is useful for suppressing an inflammatory response inhibiting composition is useful for suppressing an inflammatory response in a mammal exposed to an antigen or pathogen. An antibody that specifically binds to (I) is useful for detecting the presence of a multimeric or heterodimeric cytokine receptor in a biological sample. This sequence encodes a human zcytor17 receptors. describes an isolated multimeric or heterodimeric cytokine

Sequence 2529 B₽; 764 A; 530 C; 576 G; 659 T; 0 Ç; 0 Other;

122 488	103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 	Qy Db	
102 428	83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr :	gg Qy	
368 368	63 TYTThTGINTYTThTValLysArgThtTYrAlaPheGlyGluLysHisAspAsnCysTht (gg VQ	
62 308	43 CysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer (B &	
42 248	23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer (용 &	
22 188	3 LeuSerProGlnProSerCysValAssnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet :	gg Qy	
	65-2 (1-652) x ADL26671 (1-2529)	US-10-006-265-2	
	Alignment Scores: 4.93e-315 Fred. No.: 3441.00 Matches: 648 Fercent Similarity: 99.65\$ Best Local Similarity: 98.77\$ Query Match: 11 Gaps: Conservative: 11 Gaps: Gaps: Gaps: Conservative: 11 Gaps: Gaps: Conservative: 11 Gaps: Gap	Alignment Sc Pred. No.: Score: Score: Percent Simi Best Local S Query Match: DB:	

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 483
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NR10 splicing variants of hematopoietin receptor proteins and encoded genes, applicable in searching hematopoietic factors and developing
                                                                   WPI; 2003-018925/01.
P-PSDB; ABP54363.
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                                                                                                                                      Maeda M,
                                                                                                                                                                                                                                    26-MAR-2001; 2001JP-00087298
                                                                                                                                                                                                                                                                               22-MAR-2002; 2002WO-JP002769
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                                                       The present invention describes a cytokine receptor designated zcytor17. CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antiarthratic and muscular activities. The zcytor17 CC antirheumatic, antiarthratic and muscular activities. The zcytor17 CC proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone diagnosing lymphoid, immune, zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, cancer, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABB93843 and ABB95730 to ABB95745 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory; antivitral; antirheumatic; antiarthritic; cytostatic; muscular; lymphoid; immune; inflammatory; spleenic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
      Sequence 2386 BP;
                                          ABA93843 and ABB05730 texemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotide encoding a useful for treating and diagnosing spleenic, blood or bone disorders.
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antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic; antibacterial; immunosuppressive; cell proliferation inhibitor; immune response inhibitor; inflammatory response inhibitor; multimeric cytokine receptor; heterodimeric cytokine receptor; cancer; cytokine-binding domain; class I cytokine receptor; haematopoietic cell; zcytor171ig-induced proliferation; zcytor171ig-induced differentiation; hematopoietic progenitor cell; zcytor171ig-induced inflammation; inflammatory disease; inflammatory bowel disease; ulcerative colitis; Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia; septicaemia; toxic shock syndrome; zcytor17; human; gene; ss.
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(HAMM/) (NOVA/) (GROS/) (SPRE/) (GAOZ/) (KUIJ/) 18-JAN-2002; 2002US-0350325P. 14-JUN-2002; 2002US-0389108P. 19-DEC-2002; 2002US-0435361P. (PRES/) 21-JAN-2003; 2003US-00351157. 20-NOV-2003 (GRAN/) DILL/) DASO/) GAO Z.
) KUIJPER J L.
""" COVICH M M. DASOVICH M M.
GRANT F J.
PRESNELL S R.
WHITMORE T E.
HAMMOND A K.
NOVAK J E.
GROSS J A.
DILLON S R. SPRECHER C A.

SR, Gao Z, R Whitmore Kuijper JL, Daso ce TE, Hammond AK, Dasovich MM, Gr d AK, Novak JE, Grant FJ; Gross JA, Dillon SR;

P-PSDB; 2003-876545/81. ADL26674.

Novel multimeric or heterodimeric cytokine receptors useful for treating chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, acute inflammatory disease such as endotoxemia, septicemia.

Disclosure; SEQ ID NO 110; 205pp; English.

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The invention describes an isolated multimeric or heterodimeric cytokine receptor (I) having at least one polypeptide having 90 percent sequence cidentity with a 732 (S1) or 649 (S2) amino acid sequence given in specification, and where (I) binds a ligand comprising a 164 (S3) amino acid sequence, given in specification, or at least one polypeptide comprising residue 20-227 of (S1). (I) is useful for killing cancer cells and producing an artibody to (I) and a cytokine-binding domain of a class I cytokine receptor. A composition (C1) comprising (I) and a cytokine-binding domain of a class I cytokine receptor and a vehicle is useful for: reducing haematopoietic cells and hematopoietic progenitor cells in a mammal; inhibiting zcytor1711g-induced proliferation or differentiation of hematopoietic cells and hematopoietic progenitor cells; reducing cytor1711g-induced inflammatory disease in which zcytor1711g a mammal afflicted with an inflammatory disease such as inflammatory bowel disease is a cute inflammatory disease is acute inflammatory disease such as fortiaries for the colitis. Crohn's disease, atopic dermatitis, eczema and pservices of a content of the colitis of the colitis and the colitis and the colitis of the colitis of the colitis and the colitis and the colitis of the colitis of the colitis and the colitis of the colitis of the colitis of the colitis and the colitis and the colitis of t septicaemia, toxic shock syndrome and infectious

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                        GACAGGATCTTAAAACCATGTTCCACCCCCAGTGACAAGTTGGTGATTGACAAGTTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancytopaenia; leukopaenia; anaemia; thrombocytopaenia; ostéoporosis; neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder; cancer; myelodysplastic syndrome; idiopathic thrombocytopaenic purpura; ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
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/transl_except= (pos:1680. .1682, aa:Asn)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC treating cell proliferation conditions such as leukaemia and tumour cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone concludic and reproductive hormone concologic diseases such as cell proliferation, metabolic and reproductive hormone concologic disorders e.g. Epstein-Barr virus-positive nasopharymgeal carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, cervical and ovarian cancers, lung cancer (SCIC and NSCIC), including cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, cell, carcinoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer), compared cachexia, fatigue, solid tumours (e.g., osteosarcoma, cell carcinoma), haematologic disorders, anaemias (e.g., anaemia of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia, cell, cof chronic disease, aplastic anaemia, Fanconi's aplastic anaemia (e.g., anaemia cell valocitate fisorders that lead to bone loss such as costeoporosis including post-menopausal osteoporosis, myelofibrosis/ cesulting in tooth loosening or loss, prosthesis loosening after joint cesulting in tooth loosening or loss, prosthesis loosening after joint cerustae nervosa, chronic fatigue syndrome, transmissible dementia including Creutzfeld-Jacob disease, demyelinating neuropathy, ce myelofic as syndrome, vertebral disc disease, Gulf war syndrome, carvada mervosa, chronic fatigue syndrome, transmissible convertions and co
                                                                                                                                                                                                                                                                                                                                                                     US-10-006-265-2 (1-652)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human and murine hematopoietin receptor polypeptides HPR1 and HPR2, useful for treating cell proliferation, metabolic, and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myasthenia gravis, chronic neuronal degeneration, stroke including cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful for treating various other disorders such as osteoporosis, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 83-84; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides HPR1 and HPR2. Sequences of the invention are useful for treating cell proliferation conditions e.g., pancytopaenia, leukopaenia, treating cell proliferation conditions e.g., pancytopaenia, leukopaenia, anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis resulting from a lack of bone-forming cells. They are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAE24024.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      deficient mammary development and infertility. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention
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                                     SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro
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transgenic; gene; ss.
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/product= "GLM-R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid molecule encoding a type-1 cytokine receptor GLM-R polypeptide. The nucleic acid molecules, polypeptides, antibodies, agonists or antagonist, and compositions are useful for treating disorders characterized by the over or under abundance of monocytes or macrophages. The nucleic acid molecules are useful as hybridization probes, in chromosome and in gene mapping, and generating antisense RNA or DNA. The present sequence represents a cDNA encoding a human GLM-R polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid molecule encoding for treating disorders characterized by the monocytes or macrophages.
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The present invention describes haematopoietic receptor NR10 splicing variants (1), (1) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence encodes the human NR10.4 protein from the present invention
                                                                                                                                                                                                                 NR10 splicing variants of hematopoietin receptor proteins and encoded genes, applicable in searching hematopoietic factors and developing remedies for immunological and hematopoietic diseases.
                                                                                                                                                                                                                                                                                                                                                Maeda
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CysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer

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                                                                                                           Ly8SerProValAlaThrLeuArgIleProAlaIleGlnGluLy8SerPheGlnCy8Ile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NR10 splicing variants of hematopoietin receptor proteins and encoded genes, applicable in searching hematopoietic factors and developing remedies for immunological and hematopoietic diseases.
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                                               ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu
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  AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer
                                                                                                       HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg
                                                                                                                                             ATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATTAAATCT
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PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly
                                                          TyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn
                                                                                                                  LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer
                                                                                                                                                          AAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGGAAAAGGATTCTCC
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                                                                                                    AAGACAGTCAATTCCAGCATCTTGCAGTACGGCCTGGAGTCCCTGAAACGAAAGACCTCT
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	AAACAATTTAGGAGGGGAAAAGAATGG 2135	2109	망
	LysGlnPheArgArgGlyLysGluTrp 651	643	ş
	GTGAACTTTGGGAATGTTCTGCAAGAAATTTTCACAGATGAAGCCAGAACGGGTCAGGA-	2050	B
	ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu	623	ş
	GACAGGATCTTAAAACCATGTTCCACCCCCAGTGACAAGTTGGTGATTGACAAGTTGGTG	1990	뮹
	AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal	603	8
	ACTTCTGATTTTCTGGATAAGCTAAACCTGAAGGAGTCTGATGACTCTGTGAACACAGAA	1930	皮
	AspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu	588	Ś
	AGGTGCTGGGCTAGGCCCTAGGGATACAAATGACAAAGTCACTGTCCCTGCCATGAGGCC	1870	뭥
		587	ş
~	GGAGATGATTTCAAGGTTGGACCTCTAGAGCCGGCACTTATTAATCACTCAC	1810	뮍
	GlyAspAspPheLys	583	ş
	ACTCATCTGTGTTGGCCCACCGTTCCCAACCCTGCTGAAAGTAGTATATGCCACATGGCAT	1750	ઠ
	ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis	563	ş
	GCCTTCTTATTCTCATTATCCTGACAGTGGCATATGGTCTCAAAAAACCCCAACAAATTG	1690	망
	GlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu	543	ફ
	TTCAAGACATTGTCATTCAGTGTCTTTGAGATTATCCTCATAACTTCTCTGATTGGTGGA	1630	皮

Search completed: February 23, 2005, 09:54:04 Job time: 1031.01 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgn2 1/USPTO_spool/US1006265/runat 18022005_094658_22207/app_query.fasta_1.2069
-DB=Issued_patents_NA -QFMT=fastap_-SUFFIX=rn1 -MINMATCH=0.1 -LOOFCL=0
-LOOPEXT=0 -UNITS=5its -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human140.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15.
-LOOFEXT=0-DOCALIGN=200 -THR_SCORE=pct -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US10006265_@CGN 1 1 143 @runat 18022005_094658_22207 -NCPU=6 -ICPU=3
-NO_MFAP_LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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  first 45 summaries
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US-09-700-820C-17
US-08-795-473B-4
US-09-439-856-4
US-09-023-655-1131
US-07-797-556-1
US-08-263-1
US-09-058-263-1
US-09-058-264-1
US-09-058-264-1
US-09-455-96530-1
US-08-825-558-5
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; Patent
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	у· µ.	NO: 6610485 LL INFORMATION: CANT: Tsuchiya, Masayuki CANT: Saito, Mikiyoshi CANT: Saito, Tokibil	
	19700820C	00-820C-17 ICE 17, Application US/09700820C	Z Z '
	ALIGNMENTS		
equence 6, Appl	US-09-073-594-	44 7.0 2589	
equence 6, Appl	US-08-653-740-	44 7.0 2589	
equence 3,	US-08-347-0	8.1 249	
equence 3, Appl	US-07-943-843-3	81 8.1 2498	
equence 5, Appl	PCT-US95-06530	62 10.4 4171	
e 5, Appl	US-09-455-962-	62 10.4 4171	
equence 5,	US-09-058-264-	62 10.4 4171	
5, Appl	-660-650-60-Sn	62 10.4 4171	
5	US-09-058-263-	62 10.4 4171	
5, Appl	US-08-308-881-5	62 10.4 4171	
18	US-09-949-016-	77 10.8 4040	
Ф	US-08-914-520	77 10.8 4040	
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e 338	US-09-949-016-33	5 11.5 5252	
e 42	US-09-949-016-	11.5 5245	
e 5, App	US-08-347-003-	5 11.5 3591	
e 5, Appl	US-07-943-843-	5 11.5 3591	
1, Apr	US-08-347-003-	5 11.5 3182	
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equence	US-07-923-976-	03.5 14.5 3024	
equence 1086, F	US-09-023-655-	5 14.5 2943	
equence 3, Appl	US-07-923-976-3	05.5 14.5 2943	
equence 23, App	US-09-313-942-	6 17.7 3507	
equence 25, App	US-09-313-942-2	616 17.7 3477	
equence 3, Appl	US-09-312-611-	5 18.3 1977	
equence 3, Appl	US-08-825-558-	36.5 18.3 1977	
e 5, Appl	US-09-312-611-	77.5 19.4 2754	

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US-09-700-820C-17

i Sequence 17, Application US/09700820C

i Patent No: 6610485

GENERAL INFORMATION:

APPLICANT: Tsuchiya, Masayuki

APPLICANT: Saito, Mikiyoshi

APPLICANT: Ohtomo, Toshihiko

i TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING

FILE REFERENCE: 06501-070001

CURRENT FILING DATE: 1090-01-30

PRIOR APPLICATION NUMBER: US/09/700,820C

CURRENT APPLICATION NUMBER: UP 10/138652

PRIOR APPLICATION NUMBER: JP 10/279876

PRIOR APPLICATION NUMBER: JP 10/279876

PRIOR FILING DATE: 1998-05-20

PRIOR APPLICATION NUMBER: JP 10/279876

PRIOR FILING DATE: 1998-0-0-01

INUMBER OF SEQ ID NOS: 39

SEQ ID NO 17

LENGTH: 2995

TYPE: DNA

I ORGANISM: Mus musculus

FEATURE:

NAMEKEY: CDS

LOCATION: (29)..(2839)

US-09-700-820C-17

Alignment Scores:

Pred. No.:

SCOYE:

Alignment Scores:

Pred. No.:

SCOYE:

Alignment Similarity: 47.24%

Best Local Similarity: 47.24%

Genery Match: 19.59%

Genery Match: 19.59%

Gaps: 17
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                                                                                 1385 AAAGATAACCTGCTCTGGGTGGAATGGACACCTCCACCTAAAACCCGTGAGCAAGTACATC
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TTAGAGTGGTGTGTGTCAGAGAACGCACCTGTGTTGAAGACTGGCAGCAGGAAGAC 150
                                                                                                                AlaGluAspGlnLeuValValLysTrpGlnSerSerAlaLeuAspValAsnThrTrpMet
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                                                                                                                                                                                                              Sequence 4, Application US/08795473B Patent No. 6217858 GENERAL INFORMATION:
                                                       APPLICANT: Galun, Eithan
APPLICANT: Nahot, Orit
APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert B.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
ADDRESSEE: Davidson, Davidson and Kappel, LLC
   STREET: 1140 A-
CITY: New York
STATE: New Yor
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                                         E: Davidson, Davidson and Kappel, 1140 Avenue of the Americas
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2229

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598

1984 549 1924 489 1744

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEPAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 1036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/795,473B
FILING DATE: 11-FEB-1997
CLASSIFICATION:
                                     1063
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                                                                                                                                                                                                                                                                                                                                                  AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrTyrAlaPheGlyGlu------LysHisAsp------AsnCysThrThrAsn 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg
 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys---
                                     AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCACTGTCCAAGAC 1119
                                                                                                           AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
                                                                                                                                         ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
                                                                                                                                                                                ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG 1005
                                                                                                                                                                                                                  LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
                                                                                                                                                                                                                                                      ATCAATTTTGATCCTGTATATAAAGTG---AAGCCCAATCCGCCACATAATTTATCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                   SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACACAAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT 810
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                                                                     MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly
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LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
                                                    TTAGCATTCCTATTGACAACTCTTCTGGGAGTGCTGTTCTGCTTTAATAAGCGAGACCTA 219:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTITIACTACCCCAAAGTTTGCTCAAGGAGAAATTGAAGCCATAGTCGTGCCTGTTTGC
                                                                                                                                                                                                                      SerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
                                                                                                                                                                                                                                                                                                     SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
                                                                                                                                                                                                                                                                                                                                                                 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPhe 481
                                                                                                                                                                                                                                                                                                                                                                                                                                             ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTAATGGATCTTAAAGCATTCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg
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                                                                                                                                                                                                                                                                         GCTGTGAATGTGGATTCTTCCCACACAGAATATACATTGTCCTCTTTGACTAGTGACACA
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                                                                                          GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
                                                                                                                                                                                                   TTGTACATGGTACGAATGGCAGCATACACAGATGAAGGTGGGAAGGATGGTCCAGAATTC
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	631 CCAGAAAAACCTAAAAATTTGAGTTGCATTGTGAACGAGGGGAAGAAATGAGGTGTGAG	35	1-430-956-4 (1-3095)	/ Match: 19.50% Indels:	: 679. nt Similarity: 46.7		5	; LENGTH: 3095 Dage pairs ; TYPE: nucleic acid ; STRANDEDNESS: single	; INFORMATION FOR SEQ ID NO: 4: ; SEQUENCE CHARACTERISTICS:	10N:	REGISTRATION NUMBER: 32,728 REFERENCE/DOCKET NUMBER: 963.1007		; CLASSIFICATION: DATA: ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 08/795,473	; APPLICATION UMBER: US/09/439,856 ; FILING DATE: CINCIPLINATION.	MS-DOS EDITOR CATION DATA:	; COMPUTER READABLE FORM: ; MEDIUM TYPE: 3.5 inch disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS MS-DOS	TATE: OUNTRY	STREET: 1140 Avenue of the Americas CTTV: New York	R OF SEQUENCES: 10	TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection	, Eithan , Orit	RMATION:	856-4 A Application	2374 GATCTGAAATCATTGGACCTGTTCAAAAAGGAAAAAA	Qy 591 AsnleuLysGluSerAspAspSerValAsnThrGlu 602	Db 2314 AATTTCACTGATGTAAGTGTTGTGGAAATAGAAGCAAATGACAAAAAGCCTTTTCCAGAA 2373	Qy 590 590	Db 2254 TCACCTCACACTCCTCCAAGGCACAATTTAATTCAAAAGATCAAATGTATCCAGATGGC 2313	Qy 582 590	Db 2194 ATTAAAAAACACATCTGGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCAGTGG 2253
0у 4	Db 16:	Qy 31	Db 15	Оу 3	Db 15:	O: 50		14:	Qy 3(Qy 21	Db 131	Qy 21	QY 2.	2 11		Oy 20	10), v		Db 9,	Qy 1	DD 49	. 8	0у 1	B:	8	Db 75	ογ .	Db 69	Qy
)2 LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421	34 ATCACAGACTGGCAACAAGAAGATGGTACCGTGCATCGCACCTATTTAAGAGGGAACTTA 1713	32 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrlleGlnGlnAspLysLeu 401	94 AGGGAATCTGTAAAGAAATATATACTTGAGTGGTGTGTGT	52 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381	** TIEGILVALTECGITATICYSVALATIGGITAS DOLLEGY ALVALVYSIT STITUSTICS TO THE STITUS TO TH	11-00-11-11-11-11-11-11-11-11-11-11-11-1	22 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341	::::: ::: 4 CTGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT 1473	02 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321	32 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301 :::		52 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281	201 GLYLEUGIULEUUTPATGVALLEULYSFTOALAGUMALAASBUJYATGATGFTOVALATG 201	30 TACTIGGAGTGACIGGAGTGAAGAAGCAAGTGGGATCACCTATGAAGATAGACCATCTAAA 1239	23 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys 241	04 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222 ::: 20 CTTAAACCTTTTACAGAATATGTGTTTTAGGATTCGCTGTATGAAGGAAG		30 AGIUIIHIMAIHCIMAMAHHIMAKHIIKAKHIIKAHAHAHAHAHAHAHAHIMITHYTOVIIKAKIIIGG 1002 34 MerGluydalasnDhealaiysaanArgiysAaniysAanGlnThrTvrAsnieuThrGlv 203	54 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183	16 ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG 1005	4 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163	39 ATCAATTTTGATCCTGTATATAAAGTGAAGCCCAATCCGCCACATAATTTATCAGTG 945	2AACATTGAAGTCTGGGTAGAAGCAGAGAATGCCCTTGGGAAGGTTACATCAGATCAT 888	05 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHis 123	11 TATTCTACT 831	35 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104	751 ACACACAAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT 810	71 ThrTyrAlapheGlyGluLysHisAspAsnCysThrThrAsn 84	691 TGGGATGGTGGAAGGGAAACACCTTGGAGACAAACTTCACTTTAAAATCTGAATGGGCA 750	55 TrpSerProGlyLysGluThrSerTyrThrGlnTyrThrValLysArg 70

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US-09-023-655-1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1131, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
                                                                                                                                                                                               STREET: 31.
STREET: 31.
CITY: PALO ALTO
CTATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9186353
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DAT
APPLICATION NUMBER:
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TOPOLOGY: lir
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                                                                      LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys---
                                                                                                                                                        MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly
                                                                                                                                                                                                   AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG 1062
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                                       ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
                                                                                                                                                                                                                                                                                                                  LysProValLeuGlyIleLysArgMetIleGlnIleGlnTrpIleLysProGluLeuAla 163
                                                                                                                                                                                                                                                                                                                                                            ATCAATTTTGATCCTGTATATAAAGTG---
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                                                                                                                     AGCCAGATTCCT----CCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAGAC
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Percent Similarity:
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TELEPHONE: 206-587-0430
TELEPAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       MOLECULE AND HYPOTHETICAL: NO "WTT-SENSE: NO "Terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OF INVENTION: Inhibitory Factor
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 26
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                                                                                                                                                                                      FEATURE:
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MEDIUM TYPE: Floppy
                                                                                                                                      FEATURE
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                                                                                                       NAME/KEY:
LOCATION:
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                                                                                                                                                     LOCATION:
                                                                                                                                                                    NAME/KEY:
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                                                                                                      CTGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT
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GTAATGGATCTTAAAGCATTCCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 1581
                                                                                                                              LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu
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                                                                                                    STATE: WA COUNTRY: US ZIP: 98101
                                                                                                                                           CITY: Seattle
                                                                                                                                                      STREET:
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Sequence 1, Application US/08308881 Patent No. 5783672
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2242 TCACCTCACACTCCTCCAAGGCACAATTTTAATTCAAAAGATCAAATG
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DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-006-265-2 (1-652) x US-08-308-881-1 (1-2369)
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ATTORNEY AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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NAME/KEY:
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NAME/KEY:
LOCATION:
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ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human place
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CLONE: B10G/pDC303
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: \2007 TELEFAX: 756822
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LOCATION:
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ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG
                                                                      ATCAATTTTGATCCTGTATATAAAGTG---AAGCCCAATCCGCCACATAATTTATCAGTG
                                                                                                      MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal
                                                                                                                                        ---AACATTGAAGTCTGGGTAGAAGCAGAGAATGCCCTTGGGAAGGTTACATCAGATCAT
                                                                                                                                                                         AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His
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                  TTGTACATGGTACGAATGGCAGCATACACAGATGAAGGTGGGGAAGGATGGTCCAGAATTC 2061
                                                  SerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
                                                                                                                                                                                            ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPhe 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCACAGACTGGCAACAAGAAGATGGTACCGTGCATCGCACCTATTTAAGAGGGGAACTTA
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                                                                                                                         SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
                                                                                                                                                            CAGAATGGATTTÄTCAGAÄÄTTÄTÄCTÄTÄTTTÄTAGAACCATCATTGGÄAATGAAACT 1941
                                                                                                                                                                                                                                                                   ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu
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                                                                                                                                                                                                                                                                                                                                                                                                           LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ileGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
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                                                                                       GCTGTGAATGTGGATTCTTCCCACACAGAATATACATTGTCCTCTTTGACTAGTGACACA
                                                                                                                                                                                                                                   ACAAAAAAGTAĞĞĞAAAAACGAAGCTGTCTTAGAGTĞĞGACCAACTTCCTGTTGATGTT
                                                                                                                                                                                                                                                                                                        CCTGAATCCATAAAGGCATACCTTAAACAAGCTCCACCTTCCAAAGGACCTACTGTTCGG
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US-09-058-263-1
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                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 233-064
TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/308
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 233-0644
                                                                                                 PRAGMENT TYPE: N-term:
ORIGINAL SOURCE:
TISSUE TYPE: human |
IMMEDIATE SOURCE:
CLONE: B10G/pDC303
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
FEATURE:
NAME/KEY: mat_peptide
                                                                                                                                                                                                    MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh.
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft word, Version
CURRENT APPLICATION DATA:
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STRANDEDNESS: 81...
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                                         LOCATION:
                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/058,263 FILING DATE:
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Best Local Similarity:
Query Match:
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    302 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg 70
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                                           ACTCTCACAAGATGGAAATCACATTTACAAAATTACACAGTTAATGCCACA-----AAA
                                                                                                                                                                                                      GCACCAAGTTTCTGGTATAAAATAGATCCATCCCATACTCAAGGCTACAGAACTGTACAA 1287
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                                                                                                                       CTCGTGTGGAAGACATTGCCTCCTTTTGAAGCCAATGGAAAAATCTTGGATTATGAAGTG 1347
                                                                                                                                                            LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
                                                                                                                                                                                                                                         GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
                                                                                                                                                                                                                                                                                  TACTGGAGTGACTGGAAGTAAGAAGCAAGTGGGATCACCTATGAAGATAGACCATCTAAA 1227
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                                                                              TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
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Matches:
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Indels:
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RESULT 8
US-09-059-099-1
                                                                                                    Sequence 1, Application US/09059099
Patent No. 5925740
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin
NUMBER OF SEQUENCES: 11
                                                                                  CORRESPONDENCE ADDRESS:
                    STREET: 51 Uni
CITY: Seattle
                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                               2182 ATTAAAAAACACATCTGGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2062 ACTTTTACTACCCCAAAGTTTGCTCAAGGAGAAATTGAAGCCATAGTCGTGCCTGTTTGC
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                                                                                                                                                                                                                                                                                                                              2242 TCACCTCACACTCCTCCAAGGCACAATTTTAATTCAAAAGATCAAATG 2289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2122 TTAGCATTCCTATTGACAACTCTTCTGGGAGTGCTGTTCTGCTTTAATÅÄGCGAGACCTA 2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1882 CAGAATGGATTTATCAGAAATTATACTATATTTTATAGAACCATCATTGGAAATGAAACT 1941
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                                        E: Immunex Corporation
51 University Street
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,099
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/308,
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: TISSUE TYPE: human plac IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: N
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TELEFAX: 1256822
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ZIP: 981
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SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
                                                                                                                                                   TGGGATGGTGGAAGGGAAACACACTTGGAGACAAACTTCACTTTAAAATCTGAATGGGCA
                                                                                                                                                                                         TrpserProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg
                                                                                                                                                                                                                                                              ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
                                                                                                      ThrTyrAlaPheGlyGlu------LysHisAsp-----AsnCysThrThrAsn
                                                                  ACACACAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT
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Matches:
Conservative:
Mismatches:
Indels:
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                                                             ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu
                                                                                                                                                     ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTAATGGATCTTAAAGCATTCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 1581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCAAATCAGATGCAGCTGTTTTAACTATCCCTGCCTGTGACTTTCAAGCTACTCACCCT
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                                                                                                                     CCTGAATCCATAAAGGCATACCTTAAACAAGCTCCACCTTCCAAAGGACCTACTGTTCGG
                                                                                                                                                                                                                                                                     LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu
                                                                                                                                                                                                                                                                                                                             ATCACAGACTGGCAACAAGAAGATGGTACCGTGCATCGCACCTATTTAAGAGGGAACTTA
                                                                                                                                                                                                                                                                                                                                                                          ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACTGGAGTGACTGGAGTGAAGAAGCAAGTGGGATCACCTATGAAGATAGACCATCTAAA 1227
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Patent No. 6010886
                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/308,881
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2369 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Recepto
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOCTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                               TELEFAX: 756822
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CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2242 TCACCTCACACTCCTCCAAGGCACAATTTTAATTCAAAAGATCAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAGCATTCCTATTGACAACTCTTCTGGGAGTGCTGTTCTGCTTTAATAAGCGAGACCTA 2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp
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51 University Street
                                                                                                                                                                                             (206) 587-0430
(206) 233-0644
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LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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ORIGINAL SOURCE:
TISSUE TYPE: 1
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CLONE: B10G/pDC303
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ANTI-TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
                                                                                   1051 AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAGAC
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                                                                                                                                                                                                                                                                                                                                                      679 TGGGATGGTGGAAGGGAAACACACTTGGAGACAACTTCACTTTAAAATCTGAATGGGCA
                                                                                                                                                                                                                    124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal
                                                                                                                                                                                                                                                                                                                739 ACACACAAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT
                                                                                                                                                                                                                                                                                                                                   71 ThrTyrAlaPheGlyGlu------LysHisAsp-----AsnCysThrThrAsn
                                                                                                                                                                                                                                                                                                                                                                         55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg
                                             SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro
                                                                                                                                                              ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG
                                                                                                                                                                                                                                                        AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His
                                                                                                                         AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
                                                                                                                                    ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp
                                                                                                                                                                               LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla
                                                                                                                                                                                                                                                                             PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys---
                                                                                                    MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly
                                                                                                                                                                                                   ATCAATTTTGATCCTGTATATAAAGTG---AAGCCCCAATCCGCCACATAATTTATCAGTG
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244..2369
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29.34%
19.47%
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Matches:
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Indels:
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Ś 2002 1942 1702 1642 1522 1462 1402 1822 ACAAAAAAAGTAGGGAAAAACGAAGCTGTCTTAGAGTGGGACCAACTTCCTGTTGATGTT 1881 1582 AGGGAATCTGTÄAAGAAATATATACTTGÄGTGGTGTGTTATCAGATAAAGCACCCTGT 1641 442 302 242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541 TTGTACATGGTACGAATGGCAGCATACACAGATGAAGGTGGGAAGGATGGTCCAGAATTC GCTGTGAATGTGGATTCTTCCCACACAGAATATACATTGTCCTCTTTGACTAGTGACACA ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPhe ::: ||| ||| |||||||||||||::: ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461 CCTGAATCCATAAAGGCATACCTTAAACAAGCTCCACCTTCCAAAGGACCTACTGTTCGG 1821 GCAGAGAGCAAATGCTATTTGATAACAGTTACTCCAGTATATGCTGATGGACCAGGAAGC 1761 GTAATGGATCTTAAAGCATTCCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 1581 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361 GGCAAATCAGATGCAGCTGTTTTAACTATCCCTGCCTGTGACTTTCAAGCTACTCACCCT 1521 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys CTGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT 1461 ACTCTCACAGATGGAAATCACATTTACAAAATTACACAGTTAATGCCACA-----AAA 1401 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281 GCACCAAGTTTCTGGTATAAAATAGATCCATCCCATACTCAAGGCTACAGAACTGTACAA 1287 SerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIle SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501 CAGAATGGATTTATCAGAAATTATACTATATTTATAGAACCATCATTGGAAATGAAACT 1941 LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381 CTCGTGTGGAAGACATTGCCTCCTTTTGAAGCCAATGGAAAAATCTTGGATTATGAAGTG 1347 TCACCTCACACTCCTCCAAGGCACAATTTTAATTCAAAAGATCAAATG 2289 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581 GlyGlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561 ACTTTTACTACCCCAAAGTTTGCTCAAGGAGAATTGAAGCCATAGTCGTGCCTGTTTGC ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441 ATCACAGACTGGCAACAAGAAGATGGTACCGTGCATCGCACCTATTTAAGAGGGAACTTA ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301 TTAGCATTCCTATTGACAACTCTTCTGGGAGTGCTGTTCTGCTTTAATAAGCGAGACCTA 2181 ATTAAAAAACACATCTGGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCAGTGG HisGlyAspAspPheLysAspLysLeu 590 1701 2001 2241 521

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                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                    US-10-006-265-2 (1-652) x US-09-455-962-1 (1-2369)
                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-455-962-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09455962
Patent No. 6524817
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                       LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVIII-CENSE: NO
ANTI-SENSE: NO
TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
                                                                                                                                                                      No.:
                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: B10G/pDC303
                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 71
SOPTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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CITY: Seattle
STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/249,553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      LOCATION:
35 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
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310..2369
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244..309
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29.34%
19.47%
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678.50
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                              302 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His
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ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
                                                     AGGGAATCTGTAAAGAAATATATACTTGAGTGTGTGTGTTATCAGATAAAGCACCCTGT 1641
                                                                                                                          GTAATGGATCTTAAAGCATTCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 158:
                                                                                                                                                                                                                                                                                                                                                                                     TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
                                                                                                                                                                                                                                                                                                                                                    ACTCTCACAAGATGGAAATCACATTTACAAAATTACACAGTTAATGCCACA-----AAA 140:
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                                                                                                                                                                                                     GGCAAATCAGATGCAGCTGTTTTAACTATCCCTGCCTGACTTTCAAGCTACCTCACCCT 1521
                                                                                                                                                                                                                                                                           CTGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT 146:
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                                                                                         AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
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GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin
NUMBER OF SEQUENCES: 11
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILLING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: PSYSTEM: BC-DOS/MS-DOS SOFTWARE: Patentin Release #1, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                              STREET: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2182 ATTAAAAAACACATCTGGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCAGTGG
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1822 ACAAAAAAGTAGGGAAAAACGAAGCTGTCTTAGAGTGGGACCAACTTCCTGTTGATGTT 188:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2242 TCACCTCACACTCCTCCAAGGCACAATTTTAATTCAAAAGATCAAATG 2289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2062 ACTTTTACTACCCCAAAGTTTGCTCAAGGAGAAATTGAAGCCATAGTCGTGCCTGTTTGC
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Anderson, Kathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                     51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunex Corporation
                                                                                                                                                                                                                                                                                         Floppy disk
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Best Local Similarity:
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TELEX: 756822
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
TISSUE TYPE: human I
IMMEDIATE SOURCE:
CLONE: B10G/pDC303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: FEATURE:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                    105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyVallleLysSer---His
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                                                                                                                                                                                                                              124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal
                                                                                                                                                                                                                                                                                                                                                             85
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                   AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                  SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg
                                                          ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACACAAGTTTGCTGATTGCAAAAGCAAAAACGTGACACCCCCACCTCATGCACTGTTGAT 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrTyrAlaPheGlyGlu------LysHisAsp-----AsnCysThrThrAsn 84
                                                                                                                                             LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
                                                                                                                                                                                                                                                                       --- AACATTGAAGTCTGGGTÁGÁAGCÁGÁGÁATGCCCTTGGGAAGGTTACATCÁGATCÁT
                                                                                                        ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1522 GTAATGGATCTTAAAGCATTCCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1228 GCACCAAGTTTCTGGTATAAAATAGATCCATCCCATACTCAAGGCTACAGAACTGTACAA
542 GlyGlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg
                                                                     ACTTTTACTACCCCAAAGTTTGCTCAAGGAGAAATTGAAGCCATAGTCGTGCCTGTTTGC 212
                                                                                                                                                                                                                                                                      SerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
                                                                                                                                                                                                                                                                                                                                                      GCTGTGAATGTGGATTCTTCCCACACAGAATATACATTGTCCTCTTTGACTAGTGACACA 2001
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                                                                                                                                      AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
                                                                                                                                                                                                               TTGTACATGGTACGAATGGCAGCATACACAGATGAAGGTGGGAAGGATGGTCCAGAATTC 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĠĠĊĀĀĀTĊĀGATGCĀĠĊĪGTTŤTĀĀCTĀTĊĊĊĪĠĊĊTGTGACTTTCAAGCTACTCACCCT 152
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Percent Similarity:
Best Local Similarity:
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; LOCATION:
US-08-825-558-5
                                                                                                                                                       US-10-006-265-2 (1-652) x US-08-825-558-5 (1-2754)
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Patent No. 5965724
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SHARKEY, ANDREW
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp 130 Lacking the Transmembrane
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PATENTIN Release #1.0, VE CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/825,558

FILING DATE: 19-MAR-1997

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.05300
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)371-254
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, CONTRECT: 1100 NEW YORK AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202)371-2600
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436 TGGGATGGTGGAAGGGAAACACTTGGAGACAACTTCACTTTAAAATCTGAATGGGCA 495
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                                                                             CCAGAAAAACCTAAAAATTTGAGTTGCATTGTGAACGAGGGGAAGAAAATGAGGTGTGAG
                                                                                                    ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
                                  TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg
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Matches:
Conservative:
                                                                                                                                                                                                                 Mismatches:
Indels:
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,611
FILING DATE: 17-MAY-1999
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SHARKI
                                                                                                                                                                                                                                                  ADDRESSEE: STERNE, KESSLER, GO
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: GD130 Lacking the Transmembrane
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1939
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Best Local Similarity:
Query Match:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2754 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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STRANDEDNESS: both
TOPOLOGY: linear
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LOCATION: 1..2754
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                          GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg
                                                                                                                                                               LeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGluSerLys---
                                                                                                                                                                                                                                                                                                                                                                  ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AACATTGAAGTCTGGGTAGAAGCAGAGAATGCCCTTGGGAAGGTTACATCAGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
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GCACCAAGTTTCTGGTATAAAATAGATCCATCCCATACTCAAGGCTACAGAACTGTACAA 104
                                                                     PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys---
                                                                                                                                            AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAGAC
                                                                                                                                                                                                                                                      MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly
                                                                                                                                                                                                                                                                                                                               ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp
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Conservative:
Mismatches:
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|279 GTAATGGATCTTAAAGCATTCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 1338
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                                                                                                                                                                                                                                      TTAGCATTCCTATTGACAACTCTTCTGGGAGTGCTGTTCTGCTTTAATAAGCGAGACCTA 1938
                                                                                                                                                             HITAAAAAACACATCTGGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCAGTGG 1998
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                                                                                        TCACCTCACACTCCTCCAAGGCACAATTTTAATTCAAAAGATCAAATGTATTCAGATGGC 2058
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                                                                                                                       ----HieGlyAspAspPheLysAspLysLeu------
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Qy 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104	Oy 71 ThrTyrAlaPheGlyGluLysHisAspAsnCysThrThrAsn 84 :::	Qy 55 TrpSerProGlyLysGluThrSerTyrThrGlnTyrThrValLy8Arg 70	Qy 35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54	-825-558-3 (1-1977)	18.27% Indels: 2 Gaps:	1.94e-60 636.50 imilarity: 46.53 1 cimilarity: 26.53	•	line	ж.		· # # # #	LICATION DATA: ON NUMBER: US/08/825,558 TE: 19-MAR-1997 ATION: 536	TYPE: FI R: IBM I ING SYSTEN RE: Pater	DC UEADS	; CORRESPONDENCE ADDRESS: ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX ; STREET: 1100 NEW YORK AVENUE ; CITY: WASHINGTON	; APPLICANT: SMITH, STEPHEN K. ; APPLICANT: DELLOW, KIMBERLEY A. ; TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain ; NUMBER OF SEQUENCES: 14	MATION: SHARKEY, ANDREW	ωω	SULT 14	Qy 591 AsnLeuLysGluSerAsp
Db Qy	B &	? B 4	S B 8	? 문	8	B &	B &	B &	Qy db	QV db	D QY	Qy	ογ	Qy db	D Qy	Db QY	מם	Q	g 4g	Db
442 ValGluAsnileGiyValLyBThrValThrIleThrTrpLySGluIleProLyBSerGlu 461 	CCTGAATCCATAAAGGCATACCTTAAACAAGCTCCACCTTCCAAAGGACCTACTGTTCGG	GCAGAGAGCAAATGCTATTTGATAACAGTTACTCCAGTATATGCTGATGGACCAGGAAGC	1302 INLEGGE TERMINET VALUE CONTROLL PRODUCT OF THE	1339 AGGGAATCTGTAAAGAAATATATACTTGAGTGGTGTGTGT	362 AlaLeuAspValAsnThrTrpMetileGluTrpPheProAspValAspSerGluProThr 381	342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361 ::: ::: 1279 GTAATGGATCTTAAAGCATTCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 1338	322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341	302 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321	282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301 ::: ::	262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281	242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261	223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys 241 :::	204 LeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGluSerLys 222	184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203 :::::: 808 AGCCAGATTCCTCCTGAAGACACAGCATCCACCCGATCTTCACTGTCCAAGAC 864	164 ProvalSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183			124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143	577AACATTGAAGTCTGGGTAGAAGCAGAGAATGCCCTTGGGAAGGTTACATCAGATCAT 633	556 TATTCTACT 576

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; Sequence 3, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
APPLICANT: SHARKSY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: GP130 Lacking th
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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US-09-312-611-3
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     US-09-312-611-3
                                                                                                                                  TELEPHONE: (202)371-2600
TELEPAX: (202)371-2540
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1977 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/312
FILING DATE: 17-MAY-1999
CLASSIPICATION: 809
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTBATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
COERMATING SYSTEM: PC-DOS/
                                                                                         FEATURE:
                                                                                                                MOLECULE TYPE:
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                               NAME/KEY:
LOCATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
                                                                                                                                                                                                 ACTCTCACAAGATGGAAATCACATTTACAAAATTACACAGTTAATGCCACA-----AAA 1156
                                                                                                                                                                                                                                                  TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
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                                                                                      CTGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT 1218
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                                                                                                                                       LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
                                                                                                                                                                                                                                                                                                            CTCGTGTGGAAGACATTGCCTCCTTTTGAAGCCAATGGAAAAATCTTGGATTATGAAGTG
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Matches:
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Search completed: February 23, 2005, 19:35:55 Job time: 343.186 secs

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Command line parameters:

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-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgn2 1/USPTO_Spool/US10006265/runat_18022005_094659_22236/app_query.fasta_1.2069
-DB=PublTshed_App_ltcations_NA -QFMT=fastap -SUFFIX=rnpb -MINMAYCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US10006265_@CGN 1 1 1175_@runat 18022005_094659_22236
-NCFU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAITT-DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOD=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Ygapext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1 US-10-006-265-1

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Sequence 1, Application US/10006265
Publication No. US20030125520A1
GENERAL INFORMATION:
APPLICANT: Maeda, Masatsugu
APPLICANT: Yaguchi, No. US20030125520A11ko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001
CURRENT APPLICATION NUMBER: US/10/006,265
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/JP00/03556
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/15797
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 1
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261 ArgLe 1303 CGGTT	241 CysGl: 1243 TGTGG	221 SerLy 1183 TCAAA	201 LeuTh	181 Thrse: 1063 ACCAG	161 GluLe 1003 GAGTT	141 PheAr 943 TTCCG	121 LysSe 883 AAATC	101 IleTh 823 ATAAC	81 CYSTE 763 TGTAC	61 Thrse: 703 ACCAG	41 Ilese 643 ATTTC	21 TrpMetI 583 TGGATGO	1 MetLy 523 ATGAA	006-265-2 (1-	latch:	Alignment Scores: Pred. No.: Score: Percent Similarity:	ATION: (523)	LENGTH: 2969 TYPE: DNA ORGANISM: Homo FEATURE: NAME/YEY: CTG
uleuTrplysly GTTATGGAAGAA	YLeuGluLeuTr CCTGGAACTGTG	'sPheTrpSerAs 	rGlyLeuGlnPr GGGGCTGCAGCC	rTrpMetGluVa CTGGATGGAAGI	GluLeuAlaProValSe GAGTTGGCGCCTGTTTC	gValLysProVa TGTGAAACCAGT	LysSerHisMetThrTy 	rIleProAspAs GATCCCAGATAA	rThrAsnSerSe !AACCAATAGTTC	TYTTHTGINTY	CTGTGTCTACTA	CT C	BLeuSerF GCTCTCTC	x US-1		0 3484.00 100.00%	(2478)	sapiens
rgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAs 	ysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVa 	'9PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 	LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 	rTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 	roValSerSerAspLeuLysTyrThrLeuargPheArgThrValAsnSer 	PheArgVallysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 	.BMELThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 	IleThrileProAspAsnTyrThrileGluValGluAlaGluAsnGlyAspGlyValile 	ysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePhe 	rTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 	rCygValTyrTyrTyrArgLygAgnLeuThrCygThrTrpSerProGlyLygGlu 	roSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLys 	roGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLe 	0-006-265-1 (
aProValLeuGl CCCAGTCCTAGA	sProAlaGluAla ACCAGCTGAGGCO	uLysMetGlyMei aaaaaTGGGAAT	rValIleAlaLe TGTCATAGCTCT(sAsnArgLysAsı AACCGTAAGGA	8TyrThrLeuArg ATACACACTTCGJ	SArgMetIleGlı ACGAATGATTCAJ	uAsnIleAlaLy: GAACATAGCGAA;	uValGluAlaGlı GGTGGAAGCTGAJ	nArgAlaSerCy; CGTGCTTCGTG	gThrTyrAlaPh AACTTACGCTTT	nLeuThrCysTh: TTTAACCTGCAC	rLeuAlaAlaLe CCTGGCAGCTCT¢	lAsnLeuGlyMei TAACCTGGGGAT	(1-2969)		Length: 2: Matches: 6: Conservative: 0		
uLysThrLeuGl gaaaaCaCTTGG	aAspGlyArgAr GATGGAAGAAG	tThrGluGluGl gaCTGAGGAAGA	uArgCysAlaVa gCGATGTGCGGT	pLysasnGlnTh TAAAAACCAAAC	gPheArgThrVa ATTCAGGACAGT	nIleGluTrpIl AATTGAATGGAT	sThrGluProPr ACTGAACCACC	uAsnGlyAspGl AAATGGAGATGG	sSerPhePheLe	eGlyGluLysHi CGGAGAAAAACA	rTrpSerProGl TTGGAGTCCAGG		tMetTrpThrTr GATGTGGACCTG			969 52		
YTYFASD 280 CTACAAC 1362	gProVal 260 CCAGTG 1302	uAlaPro 240 AGCTCCA 1242	1LysGlu 220 AAGGAG 1182	rTyrAsn 200 GTACAAC 1122	lAsnSer 180 CAACAGT 1062	eLysPro 160 AAAGCCT 1002	OLYBIle 140 AAGATT 942	YValile 120 TGTAATT 882	eLeuProArg 100 CCTTCCAAGA 822	8AspAsn 80 TGATAAT 762	уLувGlu 60 АААGGAA 702	ProGluAsn 40 CTGAGAAC 642	pAlaLeu 20 GGCACTG 582					
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AAGAAATTTTCA	CCACCCCAGTG	TANACCTGAAGG	TICCCAACCCIG		TCTTTGAGATTA	ACACCAGTGCTG	TGCAGTACGGCC	CCATCTTTTACC	alThrileThri CACGATCACAT	AAGAAGGCGTTC	EFVALLYEPFOM	AGGCCACGAACT	TIGAATGGTTTC	CTGAGGACCAGC	laGluAspGlnL 	rgIleProAlaI GGATTCCAGCTA	erPheTrpValS GCTTTTGGGTGT	snLeuThrGluT ACCTCACAGAAA
CAGATGAAGCC		LUSETASPASPSETVALASI 	9=	ATGGTCTCAAA	TCCTCATAACT		TGGAGTCCCTGAAAC	AAGCTGAAGGTC	rphysGluile GGAAAGAGATTO	CATCAGAAGGTC	TGTTGCATGACA	EDITATILEGIA 	TOABDVALABDS	TAGTGGTGAAG	euValValLys:	leGlnGluLys TTCAAGAAAAA	erMetIleSer	hrMetAsnThr CAATGAACACT
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41 PheargValLysProValLeuGlYIleLYsArgMetIleGlnIleGluTrpIleLYsPro 	Qy 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140	Qy 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120	Qy 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100	Qy 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspÅsn 80 	Qy 41 IleSerCysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60	Oy 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40	Qy 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20	y Match: 99.05% Indels: 15 Gaps: 0-006-265-2 (1-652) x US-10-006-265-16 (1-2119)	Pred. No.: 0 Length: 2119 Pred. No.: 0 Matches: 650 Score: 3451.00 Matches: 1 Percent Similarity: 99.65% Conservative: 1 Best Local Similarity: 99.69% Mismatches: 1	LOCATION: (11)(1996) US-10-006-265-16	TYPE: DNA CORGANIAM: Homo sapiens FEATURE: NAME/KEY: CDS	NUMBE SOFTW SEQ ID		CURRENT APPLICATION NUMBER: US/10/006,265 ; CURRENT FILING DATE: 2003-01-06 ; PRIOR APPLICATION NUMBER: PCT/JP00/03556 ; PRIOR FILING DATE: 2000-06-01	APPLICANT: Maeda, Masatsugu APPLICANT: Yaguchi, No. US20030125520Aliko TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10 FILE REFERENCE: 06501-096001	US-10-006-265-16 ; Sequence 16, Application US/10006265 ; Publication No. US20030125520A1 ; GENERAL INFORMATION:	Oy 641 GlmGluLysGlnPheArgArgGlyLysGluTrpAsp 652
QV QV	B 8	}	S B .	S B 8	₹ B &	D Q	g Q	Qy Ob	Qy	p Q	Qy db	D Qy	p &	ОУ	Db Qy	D Qy	D Qy
501 ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520	TreserryBintvalABnserseriteLedusIntyrd.yeughenserredryBhrglyBintvalABnserseriteLyBhrglyBintyrd.yeughenserredryBhrglyBhrglyBintyrd.yeughenserredryBhrglyBintyrd.yeughenserredryBhrglyBhrglyBintyrd.yeughenserredryBhrgly	Class Control Contro		441 LVGV31G1vAsnTleG1MV43IVGTTVAlTTVSCIVGTVARGAGGTCCTGAGAAGGTCCTGAGAAGGTCCTGAGAACC 1330	LeuLyseropheTrpCysTyrAsmIlsSerValTyrPrometCeuHisAspLysValGIY	ThrThrLeuSerTrpGluSerValSerClnAlaThrAenTrpThrIleClnGlnAepLye		Cy811eGluValMetGlnAlaCy8ValAlaGluAspGlnLeuValValLy8TrpGlnSer 	321 LeuGlyLyBSerProValAlaThrLeuArgIleProAlaIleGInGluLyBSerPheGln 340 	301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320 	281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300 	261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280 	241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260 	221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240 	201 LeuThrGlyLeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGlu 220 	181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200 	161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180

Pred. No.: 2903 Score: 3451.00 Matches: 650 Percent Similarity: 99.85% Conservative: 1 Best Local Similarity: 99.69% Mismatches: 1 Query Match: 10 Indels: 1 DB: 10 Gaps: 0 US-10-006-265-2 (1-652) x US-09-892-949-53 (1-2903) Oy	TYPE: DY ORGANISH FEATURE: NAME/KEY LOCATION -09-892-94	PRIOR PRIOR PRIOR PRIOR PRIOR NUMBEI SOPTWI SEQ ID	Kuijper, Joseph L. Maurer, Mark F. NVENTION: CYTOKINE RE ENCE: 00-42 PLICATION NUMBER: US/ PLICATION NUMBER: US/ LING DATE: 2001-06-26 ICATION NUMBER: US OLICATION NUMBER: US OLICATION NUMBER: US OLICATION NUMBER: US ON DATE: 2000-06-26	US-09-892-949-53 ; Sequence 53, Application US/09892949 ; Publication No. US20030096339A1 ; GENERAL INFORMATION: ; APPLICANT: Sprecher, Cindy A. ; APPLICANT: Presnell, Scott R. ; APPLICANT: Gao, Zeren ; APPLICANT: Miltmore, Theodore E.	QY 621 Leuvalvalasnyneutyasnyalleusindjutierneimtaspiilalaktginzdy 640 Db 1871 TTGGTGGTGAACTTTGGGAATGTTCTGCAAGAAATTTTCACAGATGAAGCCAGAACGGGT 1930 QY 641 GlnGluLysGlnFrayArgGlyLysGluTpAsp 652 QY 641 GlnGluLysGlnH	1751 TGGCATGAGATGATTTCAAGGATAAGCTAAACCTGAAGGAGTCTGATGACCTCTGTGAAC 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys	OY 1 LIABRIPHE LIBERTY SINT LEUSET PRESE VALEREGIULEILE LEULLE INTESET LEULLE 540 1571 ATANATITCANGACATTGTCATTCAGTGTCTTTGAGATTATCCTCATAACTTCCTGATT 1630 QY 541 GlyGlyGlyLeuLeuIleLeuIleleleuThrValAlaTyrGlyLeuLysLysProAsn 560
5	D Q D Q	Q Q Q	D Q D Q	. OY	D 07	g	95 Qy By Qy
321 LeuGlyLysSerProValAlaThrLeuArgIIeProAlaIIeGlnGluLysSerPheGln 340	81 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 3	241 Cy8GlyLeuGluLeuTrpArgValLeuLy8ProAlaGluAlaAspGlyArgArgProVal 260	201 LeuThrGlyLeuGlnProPheThrGluTyrValIIeAlaLeuArgCysAlaValLysGlu 220	161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180	121 Ly9SerHisMetThrTyrTrpArgLeuGluAsnIleAlaLy9ThrGluProProLy8Ile 140	81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100	21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40

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Sequence 4, Application US/10351157
Publication No. US20030215838A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Gao, Zeren
APPLICANT: Kuijper, Joseph L.
APPLICANT: Kuijper, Joseph L.
APPLICANT: Basovich, Maria M.
APPLICANT: Presnell, Scott.R.
APPLICANT: Presnell, Scott.R.
APPLICANT: Hammond, Angela K.
APPLICANT: No. US20030215838A1ak, J.
APPLICANT: Billon, Stacey R.
APPLICANT: Dillon, Stacey R.
TITLE OF INVENTION: CYTOKINE RECEPTOR
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NT: Kuijper, Joseph L.

NT: Ruijper, Joseph L.

NT: Dasovich, Maria M.

NT: Grant, Francis J.

NT: Presnell, Scott.R.

NT: Whitmore, Theodore E.

NT: Hammond, Angela K.

NT: No. US2003021538A1ak, Julia

NT: Gross, Jane A.

NT: Dillon, Stacey R.

NT: Dillon, Stacey R.
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CURRENT APPLICATION NUMBER: US/10/351,157

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US 60/435,361

PRIOR FILING DATE: 2002-12-19

PRIOR FILING DATE: 2002-06-14

PRIOR APPLICATION NUMBER: US 60/350,325

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

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                   LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu
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                                                                                                        PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys
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AAATTGACTCATCTGTGTTGGCCCCACCGTTCCCCAACCCTGCTGAAAGTAGTATAGCCACA
               LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr
                                                    GGTGGAGGCCTTCTTATTCTCATTATCCTGACAGTGGCATATGGTCTCAAAAAACCCCAAC
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APPLICANT: Sprecner, Chiny C., APPLICANT: Kuijper, Joseph L. APPLICANT: Dasovich, Maria M., APPLICANT: Dasovich, Maria M., APPLICANT: Grant, Francis J., APPLICANT: Hammond, Angela K., APPLICANT: Hovak, Julia E., APPLICANT: Novak, Julia E., APPLICANT: Dillon, Stacey R., TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIGAND FILE REFERENCE: 02-01

CURRENT APPLICATION NUMBER: US/10/352,554

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US 60/350,325

PRIOR RILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-19

NUMBER OF SEQ ID NUMBER: US 60/435,315

PRIOR FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 168

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 2903

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS

LOCATION: (497)...(2482)

US-10-352-554-4
                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-352-554-4
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Publication No. US20030224487A1
GENERAL INFORMATION:
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401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420	381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400 	361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380 	341 CyBileGluValMetGlnAlaCyBValAlaGluABpGlnLeuValValLyBTrpGlnSer 360 	321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln·340 	301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320 	281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300 	261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280 1277 CGGTTGTTATGGAAGAAGGCAAGAGGAGCCCCAGTCCTAGAGAAAACACTTGGCTACAAC 1336	CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal	SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro	LeuThrdlyLeudlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 	ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200 	GluleualaprovalSerSerAspleulysTyrThrLeuArgPheArgThrValAsnSer 	141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160 	121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140 	101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120 797 ATAACGATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATT 856	81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100 	
PRIOR APPLICATION NUMBER: US 60/267,963 PRIOR FILING DATE: 2001-08-02 NUMBER OF SEQ ID NOS: 93 SOFTWARE: FASKSEQ for Windows Version 3.0 SEQ ID NO 53 LENGTH: 2903	PRIOR FILING DATE: 2001-00-20 PRIOR APPLICATION NUMBER: US 60/214,282 PRIOR FILING DATE: 2000-06-26 PRIOR APPLICATION NUMBER: US 60/214,955 PRIOR FILING DATE: 2000-06-29	FILE REFERENCE: 00-92 CURRENT APPLICATION NUMBER: US/10/772,531 CURRENT FILING DATE: 2004-02-05 PRIOR APPLICATION NUMBER: US/09/892,949	; APPLICANT: WNITHOUS, THEOROICE E. ; APPLICANT: Kuljper, Joseph L. ; APPLICANT: Maurer, Mark F. ; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17	; APPLICANT: Sprecher, Cindy A. ; APPLICANT: Presnell, Scott R. ; APPLICANT: Gao, Zeren	RESULT 6 US-10-772-531-53 ; Sequence 53, Application US/10772531 ; Publication No. US20040142422A1	Db 2417 CAGGA-AAACAATTTAGGAGGGAAAAGAATGGGAC 2451	621 LeuValValAsnPheGlyAsnValLeuGlnGluIleI	JABPATGIleLeuLy8ProCy8SerThrProSerA8pLy8LeuVallleA8pLy8 	Qy 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600	Qy 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580	Qy 541 GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLygLygProAsn 560	Qy 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540	Qy 501 ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520		LysGLyI1e11eCysAsnTyrTnr11ePneTyrG.InA1aG11G1YG1YUy9G1Y 	1817 AAGGTGGAGAACATTGGCGTGAAGACGGTCACGATCACATGGAAAGAGATTCCCAAGAGT	1757 GAGCC

Qy 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100 11	TYPE: DNA
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AAGGTGGAGAACATTGGCGTGAAGACGGTCACCATCGATAAGTGGAAAAGACGATCCCAAGAGTCACCATGGAAAAGACATTGCCAAGAGTCACCATGGAAAAGAGATTCCCAAGAGTCACATGGAAAAGAGATTCCCAAGAGTCACATGGAAAAGAGATTCCCAAGAGTCACAGAGTCACATGGAAAAGAGATTCCCAAGAGTCACAGTGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAA	281 ETPTYTYTPTOGUSETASnThrASnLeuThrGluThrMetASnThrThrASnGln 300

	Qy 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142	Qy 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122	Qy 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102	Qy 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 82	Qy 43 CysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62	Qy 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42	3 LeuSerProGlnProSerCysValAsnLe	98.77% 10) x [[S-09-892-949	J441.00 Length: 3441.00 Matches: Y: 99.85% Conservative: xity: 99.69% Mismatches:	; LOCATION: (162)(2108) US-09-892-949-45 Alignment Scores:	TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS	່ຜ		CURRENT APPLICATION OF THE CURRENT FILING PRIOR APPLICATION PRIOR FILING DAY		Sprecher, Presnell, Gao, Zere Whitmore,	-09-892-949-45 Sequence 45, Applicat Publication No. US200 GENERAL INFORMATION:	Db 2417 CAGGA-AAACAATTTAGGAGGGGAAAAGAATGGGAC 2451 RESULT 7
Ş	dg Qy	Db Db	S B ;	S B 8	S B 5	S & S	Оу	Qy db	d Q	B &	D Qy	Qу	Db Qy	D Q	g Q	Db Q	B &	υ Qγ
503 TyrīleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerīleAsn 522	483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502	AAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGGAAAAGGATTCTCC 1				LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLyeLeuLye 4	363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382 	343 GluValMetGlmAlaCysValAlaGluAspGlmLeuValValLysTrpGlmSerSerAla 362 	323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342 	303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322	283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302 	263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282 	243 LeuGluLeuTrpÄrgValLeuLysProÄlaGluAlaAspGlyArgArgProValArgLeu 262 	223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly 242 	203 GlyLeuGlnProbheThrGluTyrVallieAlaLeuArgCysAlaValLysGluSerLys 222 	TryMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThTYrAsnLeuThr 		143 VallysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162

Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Percent Similarity: Percent Similarity: Mismatches: M	; NAME / KEY: CDS ; LOCATION: (162)(2108) US-10-351-157-108	; TYPE: DNA; COMPANISM: Homo sapiens	NUMBER OF SEQ ID NOS: 183 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 108	PRIOR APPLICATION NUMBER: US 60/389,108 PRIOR FILING DATE: 2002-06-14 PRIOR APPLICATION NUMBER: US 60/350,325 PRIOR FILING DATE: 2002-01-18		APPLICANT: Gross, Jane A. APPLICANT: Dillon, Stacey R. TITLE OF INVENTION: CYTOKINE RECEPTION: CYTOKINE RECEPTION: CYTOKINE RECEPTION: DILLE DEPENATE NO.02	APPLICANT: Presnell, Scott R. APPLICANT: Whitmore, Theodore E. APPLICANT: Hammond, Angela K. APPLICANT: No. 1820003188388184 Tulia	,	Cation CAL INFO	Db 2048 AAACAATTTAGGAGGGAAAAGAATGGGAC 2077 RESULT 8 US-10-351157-108	Qy 643 LysGlnPheArgArgGlyLysGluTrpAsp 652	Qy 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642	Qy 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuVallleAspLysLeuVal 622	1869 GGAGATGATTTCAAGGATAAGCTAAACCTGAAGGAGTCTGATGACTCTGTGAACACAGAA	583 GlyAspAspPheLysAspLysLeuLssnLeuLysGluSerAspAspAspSerValAsnThrGlu 602	Qy 563 ThrHisteuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582	Db 1749 GGCCTTCTTATTCTCATTATCCTGACAGTGGCATATGGTCTCAAAAAACCCAACAAATTG 1808	1689 Trichalder Trichard Trich	Qy 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542	Db 1629 TACATTGTTCAGGTCATGGCCAGCACCAGTGCTGGGGAACCAACGGGACCAGCATAAAT 1688
323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 3	by TACTAICCAGAMAGGAACACTAACCTCACAGAAACAATGAACACTACTAACCAGCAGCTIT 03 GluLeuHisLeuGlyGlyGlyGerPheTrpValSerMetIleSerTyrAsnSerLeuGly 3 	283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 	Qy 263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282	Oy 243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262	Oy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly 242	Qy 203 GlyLeuGlnProPheThrGluTyrVallleAlaLeuArgCy8AlaValLy8GluSerLy8 222	Qy 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202	Qy 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182	Qy 143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGlnTrpIleLysProGluLeu 162	Qy 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142	429 ATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGAGGTGTAATTAAATCT	AGTTCTACAAGTGAAAATCGTGCTTCGTGCTCTTTTTTTCCTTCC	Db 309 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACA 368 Oy 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102	63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 8	249 TGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAAACCAGT 3	TCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAAAC	LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnTleSer 42	Qy 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpThlaLeuTrpMet 22	US-10-006-265-2 (1-652) x US-10-351-157-108 (1-2529)	Query Match: 98.77% Indels: 1 DB: 17 Gaps: 0

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RESULT 9
US-10-772-531-45
US-10-772-531-45
Sequence 45, Application US/10772531
Publication No. US20040142422A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
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APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/10/772,531
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/9/892,949
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-66-29
PRIOR FILING DATE: 2000-66-29
PRIOR FILING DATE: 2000-66-29
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOTTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 45
LENGTH: 2529
TYDER: DNA
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 GGCCTTCTTATTCTCATTATCCTGACAGTGGCATATGGTCTCAAAAAACCCAACAAATTG
           GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu
                                                       TyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn
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; Sequence 5, Application US/09972708
; Publication No. US20030059871A1
; GREERAL INFORMATION:
; APPLICANT: Inmunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Wiley, Steven R.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 ANI
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Alignment Scores: Pred. No.: 91.00 Alignment Scores: 18	541 GlyGlyGlyLeuLeulleLeullelleuThrValhaTyrGlyLeuLysLysProAsn [621 GGTGGAGGCCTTCTTATTCTCATTATCCCTGACAGTGGCATATGGTCTCAAAAAACCCAAC 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr [681 AAATTCATCTATTCTGTGTTTGCCCGGTTGCCATATGGTCTCAAAAAACCCAAC 561 TrpH.sGlyAspAspAspHeLysAspLysLeuAsnLeuLysGluSerSerIleAlaThr [681 AAATTCATCTATCTGTGTTTGCCCGGTTGCCACCCTTGCTGAAAGTAGGTATAACCCAAC 581 TrpH.sGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn [741 TGCCATGGAATGATTTCAAGGATAAACCTAAACCTGAAGGAGTCTGATGACTCTGTGAAC 601 ThTGluAspArglleLeuLysProCysSerThrProSerAspLysLeuVallaspLys [741 TGCCATGGAAGTGATTTCAAGGATAAACCTAAACCTGAAGGAGTCTGATGACTCTGTGAAC 602 LeuValValAspArglleLeuLysProCysSerThrProSerAspLysLeuVallaspLys [741 TGCCATGGAAGTGATTTCAAGGATAAACCTAAACCTTAACCCCCCAGTGACAGTTGGTCATTGACAAG 603 ACAGAAGAACAGATTTAAAACCATGTTCCACGAAGAGTTGAAGTTGACAAG 604 CAGAAGAACAAGAATTAAAACCATGTTCCAAGAAAATTTTCACAAGTTGAACCAGG 605 LeuValValAspArglleLeuLysProCysSerThrProSerAspLysLeuVallalArgThrGly [751 Hill	Qy 461 GluArgLy8GlyIleIleCy8AsnTyrThrIlePheTyrGlnAlaGluGlyGlyLy8Gly 480

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RESULT 12
US-09-892-949-1
US-09-892-949-1
Sequence 1, Application US/09892949
Publication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Muliper, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZC
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; TYPE: DNA; ORGANISM: HOMO BADI; FEATURE: RAME/KEY: CDS; LOCATION: (171)...(US-09-892-949-1
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CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FRBESEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2402
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        ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
                                          LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
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                                                                                                                         TyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn
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Qy 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62	Qy 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42	Qy 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22	S-10-006-265-2 (1-652) x US-10-351-157-110 (1-2402)	t Similarity: 99.85% Conservative: 1 ocal Similarity: 99.69% Mismatches: 1 Match: 98.59% Indels: 1	Length:			NUMBER SOFTWA SEQ ID		CURRI	INC A. STACEPTOR ECY TOKINE RECEPTOR ECY	APPLICANT: Presnell, Scott R. APPLICANT: Whitmore, Theodore E. APPLICANT: Hammond, Angela K. APPLICANT: No. IIS20010215838A1ak Julia E	APPLICANT: Gao, Zeren APPLICANT: Kuijper, Joseph L. APPLICANT: Dasovich M. APPLICANT: Grant Prancis I	; Sequence 110, Application US/10351157 ; Publication No. US20030215838A1 ; GENERAL INFORMATION: ; APPLICANT: Sprecher. Cindy A.	SULT 13 -10-351-157-110	Qy 643 LysGlnPheArgArgGlyLysGluTrp 651	Db 1998 GTGAACTTTGGGAATGTTCTGCAAGAAATTTTCACAGATGAAGCCAGAACGGGTCAGGA- 2056	623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu	Qy 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuVallIeAspLysLeuVal 622	Db 1878 GGAGATGATTCAAGGATAAGCTAAACCTGAAGGAGTCTGATGACTCTGTGAACACAGAA 1937
- dg	? D &	} B &	B	Qy Qy	Qy	D Q	da Vy	D Qy	Db Qy	Db Qy	ДУ	Qу	Qу	ОУ	Db	ον Db	Qy	Db	O Db	δ β
1338 CCTTTCTGGTGCTATAACATCTCTGTGTATCCAATGTTGCATGACAAAGTTGGCGAGCCA 1397		Leuas by alasmini i prec'i legini i breriona y alasbetisio i colini i leuas by alasmini i prec'i legini i breriona y alasbetisio i colini i legini		1098 AAGTCTCCAGTGGCCACCCTGAGGATTCCAGCTATTCAAGAAAAATCATTTCAGTGCATT 1157 343 GluvalMetGlnAlaCysVallHll	323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342	303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322	283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302 	263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282 	243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262 	223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly 242	203 GlyLeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGluSerLys 222 	183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAspGnThrTyrAsnLeuThr 202 	163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182 	143 VallysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162 		438 ATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATTAAATCT 497 123 HigMetThrTyrTroArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142	IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer		318 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAAACATGATAATTGTACA 377 83 ThraenSerSerThrSerGluaenargalaSerCyeSerPhePheLeuProargIleThr 102	258 TGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGICCAGGAAAGGAA

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RESULT 14

US-10-772-531-1

Sequence 1, Application US/10772531

Publication No. US20040142422A1

REMERAL INFORMATION:

APPLICANT: Sprecher, Cindy A.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Kuijper, Joseph L.

APPLICANT: Maurer, Mark F.

TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17

FILE REFERENCE: 00-42

CURRENT APPLICATION NUMBER: US/10/772,531

CURRENT APPLICATION NUMBER: US/9/892,949

PRIOR APPLICATION NUMBER: US 60/214,282

PRIOR FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: US 60/214,955

PRIOR APPLICATION NUMBER: US 60/214,955

PRIOR APPLICATION NUMBER: US 60/267,963

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/267,963

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 93
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; SEQ ID NO 1
; LENGTH: 2402.
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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   LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp
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                                                   LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu
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ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu
                                                                       AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal
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US-09-972-708-3

US-09-972-708-3

Sequence 3, Application US/09972708

Publication No. US20030059871A1

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Cosman, David J.

APPLICANT: Mosley, Bruce A.

APPLICANT: DuBose, Robert F.

APPLICANT: DuBose, Robert F.

APPLICANT: Wiley, Steven R.

TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2

FILE REFERENCE: 3160-B

FILE REFERENCE: 3160-B

CURRENT APPLICATION NUMBER: US/09/972,708

CURRENT FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 2480

TYPE: DNA

ORGANISM: Homo sapiens
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REFERENCE AUTHORS REFERENCE
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AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AK030512 LOCUS DEFINITION JOURNAL MEDLINE PUBMED TITLE Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P. Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishir, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253 AK030512 2232 bp mRNA Mus musculus adult male pituitary gland enriched library, clone:5330424C19 produ Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Mus musculus Mus musculus (house mouse) AK030512.1 GI:26326508 10349636 HTC; CAP trapper. full insert sequence. 11042159 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus gland cDNA, RIKEN ful: product:hypothetical linear HTC 03-APR-2004 full-length Carninci, P., protein, genes

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Analysis of the mouse transcriptome of 60,770 full-length CDNAs
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Functional annotation of a
Functional 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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                                                                              /proteIn_id="BAC26998.1"
/db_xref="G1:26326509"
/db_xref="G1:26326509"
/translation="MASTRAGGTNGVRINFKTLSISVFEIVLLTSLVGGGLLLLSIKT
/translation="MASTRAGGTNGVRINFKTLSISVFEIVLLTSLVGGGLLLLSIKT
VTFGLAKENRLIPLCCEDVPNEAESSLATWLGDGFKKSNMKETGNSGDTEDVVLKPCP
VPADLIDKLVVNFENFLEVVLTEEAGKGQASILGGEANEYVTSPSRPDGPPGKSFKEP
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/clone_lib="RIKEN full-length enriched mouse
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/db_xref="taxon:10090"
/clone="5330424C19"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5264)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler, Klausner,R.D., Collins,F.S., Buetow,K.H., Schaefer,C.F., Bhat,N. Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N. Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F. Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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Matches:
Conservative:
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frame-shift
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                                               Bhat, N.K.,
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                               581
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Email: cgapbs-r@mail.nih.gov

Tissue procurement: Miklos Palkovits, M.D., Ph.D.

Tissue procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI) &

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human of Center, Stanford University School of Medicine, Stanford, Web site: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 167 Row: a Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28610146
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                          TrpSerProGlγLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg 70
                                                                                                                                                                            ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
                             TGGGATGGTGGAAGGGAAACACACTTGGAGACAAACTTCACTTTAAAATCTGAATGGGCA 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4374041"
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/lab_host="DH10B"
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ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
                                                  GCAGAGAGCAAATGCTATTTGATAACAGTTACTCCAGTATATGCTGATGGACCAGGAAGC 1663
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                                                                                                                                                                                                                                                      AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
                                                                                                                                                                                                                                                                                                                                                        GTAATGGATCTTAAAGCATTCCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 148:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCACCAAGTTTCTGGTATAAAATAGATCCATCCCATACTCAAGGCTACAGAACTGTACAA 1189
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                                                                                               LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
                                                                                                                                                                                                   ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
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RESULT 3
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Xu.C.S., Li.W.Q., Li.Y.C., Han,H.P., Wang,G.P., Chai,L., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Liver regeneration after PH
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Rattus norvegicus Ac1055 mRNA,
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AY310138.1 GI:32264598
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Rattus norvegicus (Norway
                                                                                                      Submitted (29-MAY-2003) Henan Bioengineering Key Lab, Henan No. University, No. 148 Jianshe Road, Xinxiang City, Henan 453002,
                                                                                                                                              Wang, L., Wang, S.F.
Direct Submission

    (bases 1 to 3055)
    Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q.,
    Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
    Yuan,J.Y., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.

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/organism="Rattus norvegicus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                          AlaGluAsnGlyAspGlyValIleLysSerHisMetThrTyrTrpArgLeuGluAsnIle 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheGlyGluLysHisAspAsnCysThrThrAsnSerSerThrSerGluAsnArgAlaSer
      GTGTCTCCCCGGACTTCGTTCACTGTTCAGGATCTCAAGCCTTTTACAGAATATGTGTTT
                         LysAspLysAsnGlnThrTyrAsnLeuThrGlyLeuGlnProPheThrGluTyrValIle :::::: :::
                                                                                     ATCCAATATAGGACCAAAGATGCCTCAACTTGGATTCAGGTCCCTCTT---GAAGATACA
                                                                                                                 LeuArgPheArgThrValAsnSerThrSerTrpMetGluValAsnPheAlaLysAsnArg
                                                                                                                                                                    TTAAAACTAGCATGGGTCAATTCAGGTTTTGGACAGTATTTTAAGG----CTGAAGTCGGAC
                                                                                                                                                                                                          IleGlnIleGluTrpIleLysProGluLeuAlaProValSerSerAspLeuLysTyrThr
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                                                                                                                                                                                                                                                                                                                                      GCCGAGAATGCCCTTGGGAATGTCTCCTCAGAGCCTATCAATTTTGACCCCCGTGGATAAA
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DLKPFTEYVFRIRSIKENGKCYWSDWSEEASCTTYEDRPSKAPSFWYKWAMHPQEYR
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SCSCSQPGASPDVSHFERSSQVPSGSSEBDFVALKQQOVSDHISBPYGSSQRRLFQEGSV
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QNVYGITILSGYPPDIPTNLSCIVNEGKNMLCQWDPGRETYLETNYTLKSEWATEKFP
DCRTKHGTSSCMMGYTPIYFVNIEVMVEAENALGNVSSEPINFDPVDKVKPSPPHNLS
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LVLIVDRPPEVQDSSQRTQLEHKLRQLHAHSLSNKLELNSFNQSPDGQASSQSEPTAF
SSVNRRDTPVDIWHSQVKTKMATENWTNSSSFFHPCKE"
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/db_xref="taxon:10116"
17. ...3049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="liver regeneration
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647.50
45.64%
28.82%
18.58%
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185
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700 152 640

580

LysPro 559 	50	185
IleIle 549 ::: GCCGTA 1852	30 ValPheGluIleIleLeulleThrSerLeulleGlyGlyGlyLeuLeuIleLeulleIle 	530 1811
Pheser 529 TTTGGT 1810	10 ABNThrSerAlaGlyGlyThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSer	51 175
MetAla 509 GCAGCA 1750	90 LeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSerTyrIleValGlnValMetAla 	49 169
SerIle 489	70 ThrilePheTyrGlnAlaGluGlyGlyLysGlyPheSerLysThrValAsnSerSerIle	470 1631
ABnTyr 469 AACTAC 1630	50 ValThrIleThrTrpLysGluIleProLysSerGluArgLysGlyIleIleCysAsnTyr :::	450 1571
LysThr 449 WAATGAA 1570	30 LysGluGlyValProSerGluGlyProGluThrLysValGluAsnIleGlyValLysThr ::: ::: :::	430 1511
TyrAla 429 TACCTC 1510	10 SerValTyrProMetLeuHisAspLysValGlyGluProTyrSerIleGlnAlaTyrAla 	410 1451
AsnIle 409 CTGATC 1450	90 GlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLysProPheTrpCysTyrAsnIle 	39 139
:ValSer 389 \GAAGAT 1390	70 IleGluTrpPheProAspValAspSerGluProThrThrLeuSerTrpGluSerValSer 	37 133
TrpMet 369 :::::: TACATA 1330	50 AlaGluAspGlnLeuValValLysTrpGlnSerSerAlaLeuAspValAsnThrTrpMe	35 127
CYSVAL 349 ATTTCCA 1270	30 ArgIleProAlaIleGlnGluLy8SerPheGlnCy8IleGluValMetGlnAlaCy8Val	33 122
ThrLeu 329 GTCCTC 1225	10 SerPheTrpValSerMetlleSerTyrAsnSerLeuGlyLysSerProValAlaThrLeu 	31 116
⁄GlyGlu 309 XAATAAC 1165	90 AsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeuGluLeuHisLeuGlyGlyGlu ::: :::	290 1112
AsnThr 289 ::: TCAGTT 1111	70 AlaProValLeuGluLysThrLeuGlyTyrAsnIleTrpTyrTyrProGluSerAsnThr :::	27 105
ArgGly 269 SCCCCTT 1051	50 LysProAlaGluAlaAspGlyArgArgProValArgLeuLeuTrpLysLysAlaArgGly 	99
yValLeu 249 ∶:: rAAGGTA 991	31 Ly8MetGlyMetThrGluGluGluAlaProCy8GlyLeuGluLeuTrpArgValLeu 	93
cGlnGlu 230 ::: GAGGAG 931	13 AlaLeuArgCysAlaValLysGluSerLysPheTrpSerAspTrpSerGlnGlu 	21 87

JOURNAL COMMENT	D	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 4 BB617934 LOCUS DEFINITION	9g 4 g	, 4d	gb Qy	Qγ :	Qy Db :	QQ YQ
Contact: Yoshihide Hayashizaki Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci.p. Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res 11 (2), 281-289 (2001) Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shibata,K., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,	Arakawa, T., Can Hara, A., Hiramc Konno, H., Koudd Ohno, M., Okazaki Sano, H., Sasaki Sogabe, Y., Suzu Takeda, Y., Tana RIKEN Mouse EST	musculus cDNA clone 5330424C19 5', mRNA sequence. BB617934 BB617934.1 GI:15396442 EST. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri	BB617934 RIKEN full-length enriched, and	650 GluTrp 651 2137 CAGTGG 2142	630 GlnGluIlePheThrAspGluAlaArgThrGlyGlnGluLysGlnPheArgArgGlyLys 649 	610 SerThrProSerAspLysLeuVallleAspLysLeuValValAsnPheGlyAsnValLeu 629 	591 ABRLEULYBGluSerABpABpSerValABRThrGluABpArgIleLeuLyBProCyB 609 	580 ThrTrp 590	560 AsnLysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAla 579

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 ProSerGluGlyProGluThrLysValGluAsnIleGlyValLysThrValThrIleThr
                                                                      534 IleLeuIleThrSerLeuIleGlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAla 553
                                                                                                                                                             514 GlyGlyThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSerValPheGluIle
                                                                                                                                                                                                                      392
                                                                                                                                                                                                                                                494 LeuGluSerLeuLysArgLysThrSerTyrIleValGlnValMetAlaAsnThrSerAla
                                                                                                                                                                                                                                                                                                                                    474 GlnAlaGluGlyGlyLysGlyPheSerLysThrValAsnSerSerIleLeuGlnTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                             454
554 TyrGlyLeuLysLysProAsnLysLeuThrHisLeuCysTrpProThrVal-ProAsnPr 573
                                                                                                                                                                                                                                                                                                             332 CAAGCTGAAGGTGGAAAAGAACTCTCCAAGACTGTTAACTCTCATGCCCTGCAGTGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                  272 TGGAAGGAGATTCCTAAGAGTGCTAGGAATGGATTTATCAACAATTACACTGTATTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 CCATTAAAAGGTCCTGAGACCAGGGTGGAGAACATCGGTCTGAGGACAGCCACGATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arakawa,T., Ishii,Y. and Hayashizaki,Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.

Punc. Genomics 2 pre, L72-L86 (2001

Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                           TrpLysGluIleProLysSerGluArgLysGlyIleIleCysAsnTyrThrIlePheTyr
                                           GTCCTTCTAACATCTCTAGTTGGAGGAGGCCTTCTTCTACTTANCATCAAAACAGTGACT
                                                                                                                                GGAGGTACCAACGGGGTGAGAATAAACTTCAAGACATTGTCAATCAGTGTGTTTGAAATT
                                                                                                                                                                                                                      CTGGAGTCTCTGACACGAAGGACCTCTTATACTGTTTGGGTCATGGCCAGCACCAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 3.0 and subtraction to Rot = 10.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCTCGAGTTAATTAATTCACCCCCCCCC3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pituitary gland"
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/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
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526.00
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RESULT 5
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1 (bases 1 to 653)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)

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BU455838
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Department of Biomolecular Sciences
University of Manchester Institute of
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/clome_lib="CSEGRBN14"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
/constructed from 1 million independent clones: cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI; size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KG+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simon Hubbard@umist.ac.uk
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/lab_host="DH10B"
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/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Layer"
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384 SerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLysPro 403

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B0932D09-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
musculus cDNA clone NIA:B0932D09 IMAGE:30475340 5', mRNA sequence.
CP174021
CP174021.1 GI:33283570
                                                                                    Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
33 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnæelgsun.grc.nia.nih.gov
Plate: B0932 row: D Column: 09
Seq primer: M13 Reverse
High quality sequence stop: 637
                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 637)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="niaEST:B0932D09-5" /db_xref="taxon:10090" /db_xref="Union:10090" /clone="NIA:B0932D09 IMAGE:30475340" /dev_stage="Union:Inized Egg" /lab_host="Union: Union:Inized Egg cDNA Library (Long /lone_lib="NIA Mouse Union:Inized Egg cDNA Library (Long I)" /site_: NotI, Mouse CDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pgAGCTAGTTGTGAGGGGGGGGGGGCCCCTTTTTTTTTTTT
Double-stranded CDNAs were Synthesized with an Oligo (dT) primer [Invitrogen: 5'-pgAcTAGTTCTAGATCGCGAGCGGCCCCTTTTTTTTTTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by Phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pcMV-SpORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."
ont Scores: 1.58e-39 Length: 637 No.: 468.50 Matches: 96 Similarity: 63.59\$ Conservative: 21 coal Similarity: 52.17\$ Mismatches: 53 Vatch: 13,45\$ Indels: 13
006-265-2 (1-652) x CF174021 (1-637)
7 ProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSerLeu 26
27 CYSLYSPHeSerLeuAlaAlaLeuProAlaLySProGluAsnIleSerCysValTyrTYr 46
47 TyrarglybabnleuThrCybThrTrpSerProGlyLybGluThrSerTyrThrGlnTyr 66 ::: :::
67 ThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThrThrAsnSerSer 86
87 ThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
105 ASPASNTYrThrIleGluValGluAlaGluAsnGlYASpGlYValIleLy8SerHisMet 124
125 ThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgValLys 144
145 ProValLeuGlyIleLy8ArgMetIleGlnIleGluTrpIleLy8BroGluLeuAlaPro 164

Direct Submission

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N. Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N. Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S. Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                        Group Phase I & II Team.
Analysis of the mouse transcriptome
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2804)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria;
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Sciurognathi; Muridae;
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; Murinae; Mus.
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                                                                                                     Sakazume, N.,
                                                                                                                                                                                                                                                                                      Carninci, P.
                                                                                                                            Ohsato, N.,
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GS RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yok Kanagawa 230-0045, Japan (E-mail:genome-ree@gc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assistance we gratefully acknowledge. Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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                                 ProValLeu--
                                                                                CTCGACCCCATGGATGTTGTGAAATTGGAGCCTCCCATGCTGCAGGCCCTGGACATTGGC
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                                                                                                                                                                                 ATGGCCATCTGGGTGCAAGCAGAGAATATGCTAGGGTCCAGCGAGTCCCCAAAGCTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                      AGCTTCAGGAGCCGCCCGAC---TGTCAGTACCAAGGGGACACCATCCCGGATTGTGTG
                                                                                                                                                                                                                                  TyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHisMetThrTyr
                                                                                                                            TrpArgLeuGluAsnIleAlaLysThrGluProProLysIle-----PheArgValLys 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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(MGD|MGI:1339755,
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/cell_type="B6-derived CD11 +ve dendritic cells"
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/db_xref="taxon:10090"
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r55, GB|NM_007782, evidence: BLASTN, 99%,
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     -GlyIleLysArgMetIleGlnIleGluTrpIleLys 159
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AlaGluGlyGlyLysGlyPheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeu 494
                                                                                            GTACCTGAGGCCCCTAGGCTGGGGATGATACCCCTCACCCACTACACCATCTTCTGGGCC 1911
                                                                                                                                                                                                                                GlyProGluThrLysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGlu 456
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                                                                                                                                                                                         GCTCCAGCGCTGCATCTAAAGCATGTTGGCACAACCTGGGCACAGCTGGAGTGG-----
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                                                                                                                                                                                                                                                                                                                               AspLysValGlyGluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGlu 436
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                                                                                                                                        IleProLysSerGluArgLysGlyIleIle-----CysAsnTyrThrIlePheTyrGln 474
                                                                                                                                                                                                                                                                                   GluThrMetAsnThrThrAsnGlnGlnLeuGluLeuHisLeuGlyGlyGluSerPheTrp
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CysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSerLeuCysLys

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KEYWORDS
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US-10-006-265-2 (1-652) x AY412152 (1-2592)
                                                     Query Match:
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Best Local Similarity:
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Toodd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2592)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Science 302 (5652), 1960-1963
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                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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                                                                                                                                                                                                                                                                                                                                                            sequence was made by sequencing based on alignment.
                                                                                                                                                                                              <1...>2592
/gene="CSF3R"
/locus_tag="HCM4462"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AlaproCysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAla 25	29 PheSerLeuhlaAlaLeubroAlaLysproGlumsnIleSerCysValTyrTyrTyrTyr 48 29 PheSerLeuhlaAlaLeubroAlaLysproGlumsnIleSerCysValTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrT
RESULT 9 BC040954 LOCUS BC040954 LOCUS DEFINITION MRNA (cDNA clone IMAGE:5588879), containing frame-shift errors. ACCESSION RC040554 BC040554 BC04056	351 GlubspGlinienvalvaliysTrpGlinserSerAlaLeuAspValAsnThrTrp 368 1318 CGAGACCCTCACAGCCTCTGGGTAGGCTCGGAGGCCCCC

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DB: US-10-006-265-2 QY 9 C Db 397 T QY 29 P Db 442 C QY 49 L Db 490 A OY 64 -	Source Source Source IGIN IGIN Sed. No.: bed. No.: bed. No.: bed. No.: arcent Sim St Local Sim Sery Match	TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REMARK COMMENT
Gaps: x BC040954 (1-2792) LeuGlyMetMetTrpThrTrpAlaLeuTrp	ribution: MGC clone distribution information e I.M.A.G.E. Consortium/LLNL at: http://im.AK Plate: 84 Row: i Column: 2 was selected for full length sequencing be following selection criteria: matched mRN. has the following problem: frame shifted. ocation/Qualifiers2792 organism="Homo sapiens" mol_type="MNAGE:5588879" tissue_type="Ovary, pooled from 3 adults" clone="TMAGE:5588879" tissue_type="Ovary, pooled from 3 adults" clone="TMAGE:558879" tissue_type="Ovary, pooled from 3 adults" tissue_type="Ovary, pooled from 3 adults" tissue_type="TMAGE:558879" tissue_type="TMAGE:558879" tissue_type="TMAGE:558879" tissue_type="TMAGE:558879" tissue_type="TMAGE:5	Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Scheutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257 [Chaeses 1 to 2792) [Chaeses 1 to 2792) [Chaeses 1 to 2792] [Chaeses 1 to 27
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1138 CTCAGCCGGGACCTCTCGTCCCACTCCGGTGGTCTTCTCAGAAAGCAGAGGCCCAGCTCT 1197 334 eGlnGluLysSerPheGlnCysIleGluValMetGlnAlaCysValAlaGluAsp 352 :	200 ASDLEUTHTGLYLEUGINPTOPHETHTGLUTYYVALLEALALEUATGCYS ALAVALLY 219 219 GAGCTCTGCCGGGCTCCTCCCAGCCACCGCCTACACCCTGCAGATACGCTGCAGTCCGCT 1027 219 SGLUSERLYSPHETTPSETASPTTPSETGINGLULYSMETGLYMETTHTGLUGLUAL 239 1028	

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                                                                                                                                                                                                                                                                                                                                                                                                                                     CF915066 651 bp mRNA linear EST 05-NOV-200 E0973F04-5 NIA MOUSE Unfertilized Egg cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0973F04 IMAGE:30479295 5', mRNA sequence. CF915066 CF915066.1 GI:38186268
                    Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, t
Email: cdnaglgsun.grc.nia.nih.gov
Plate: B0973 row: F column: 04
                                                                                                                                                                                                                                                                                    Piao,
                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                 11544199
Contact: Dawood B.
                                                                                                                                                                                              Genome Res. 11 (9), 1553-1558 (2001)
                                                                                                                                                                                                                                      submicrogram amounts of total RNAs by a universal PCR amplification
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High quality sequence stop: POLYA=No.
                                                                                                                                                                                                                                                                 treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="NIA:B0973F04 IMAGE:30479295"
/dev_stage="Unfertilized Egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer (Invitrogen:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
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52.32%
11.39%
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Conservative:
Mismatches:
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564	505 CCAGACATCTGCAGTGTTGAAGTTACAAGCTCAAAATGGAGATGGTAAAGTTAAATCTGAC 564	505	Дb
123	ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHis		S S
504	445 AATTATAGTGACAATGCTACAGAGGCTTCATATTCTTTTCCCCCGTTCCTGTGCAATGCCC 504		밁
103	SerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIle 103		Ş
444	409 TACATTGTGACTTTGACTTACTCCTATGGAAAAAGC 444	409	망
85	66 TyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThrThrAsnSer 85	66	Ş
408	TACTTCGACAGAAATCTGACTTGCACTTGGAGACCAGAGAAGGAAACCAATGATACCAGC	349	뮍
65	46 TyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGln 65	46	Ş
348	CTCTGCAAATTCAGCCTGGCAGTCCTGCCGACTAAGCCAGAGAACATTTCCTGCGTCTTT	289	дb
45	26 LeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSerCysValTyr 45	26	Ş
288	CAGCCTCTGGGTGTGAACGCTGGAATAATGTGGACCTTGGCACTGTGGGCATTCTCTTTC	229	ਰੂ
25	G GlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSer 25		Ş
	US-10-006-265-2 (1-652) x CF915066 (1-651)	-10-006-265	SD

Indels:

8	8 8	B 8	Qy Db	DB: US-10-006-265	Pred. No.: Score: Percent Simi Best Local S Ouery Match:	ORIGIN Alignment	9		FEATURES source	COMMENT	TITLE JOURNAL	AUTHORS	JOURNAL PUBMED REFERENCE	TITLE	AUTHORS	REFERENCE	SOURCE	VERSION VERSION KEYWORDS	LOCUS	RESULT 11 AY412154	Db	8	qq	ş
88SerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIleProAspAsn 106	73 AlaPheGlyGluLysHisAspAsnCysThrThrAsnSerSerThr	54 ThrTrpSerProGlyLysGluThrSerTyrThrGlnTyrThrValLysArgThrTyr 72	35 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCys 53	9 Gaps: -2 (1-652) x AY412154 (1-2535)	1.16e-30 395.50 larity: 39.80% imilarity: 25.33% inilarity: 11.35%	Scores:	/gene_"CSF3R" /locus_tag="HCM4462"	/molltpe="genomic DNA" /db_xref="taxon:10090"	e 12535 'Organism."Mis miscrilis"	ville, MD 20850, USA Bequence was made by sequencing genomic exons and	Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,	lark, A.G., Gla odd, M.A., Tane erriera, S., Wa dams, M.D. and	gene Lilo Science 302 (5652), 1960-1963 (2003) 14671302 2 (bases 1 to 2535)	and Cargill,M. nonneutral evolution from huma	CLETK, A.G., GLENOWSKI, S., NIELSON, K., TROMMS, P., KEJETIWAL, A., TONGHDAUM, D.M., CIVELIO, D.R., LU, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,	Metazoa; Chordata; Craniata; Vertebrata; Euteleo utheria; Rodentia; Sciurognathi; Muridae; Murina to 2535)	Mus musculus (house mouse)	AY412154 AY412154.1 GI:39768119 GSS.			625 AATCCAATTTGTAATAGAATGTTCCAG 651	144 LysProValLeuGlyIleLysArgMetIleGln 154	ATCACATATTGGCATTTAATCTCCATAGCAAAAACCGAACCACCTATAATTTTAAGTGTG	124 MetThrTyrTrpArqLeuGluAsnIleAlaLvsThrGluProProLvsIlePheArqVal 143
B 8	B &	\$ \$ \$? B &	рь	δ β δ	Db	Q G	ş &	da K	당 당 당	ρ	Qy db	D Q	? B	Q	оу оь	Dъ	ρ	Qy Db	Db	Ş	DЬ	Q (₽
409 IleSerValTyrProWetLeuHisAspLysValGlyGluProTyrSerIleGlnAlaTyr 428 :::	AACGGGAACATCACTGGAATTCTGTTAAAGGACAACATAAATCCCTTTCAGCTCTACAGA		65 ValasnThrTrpMetileGluTrpPheProAspValAspSerGluProThrThrLeu ::: 62 CTTAACACCATCTGGGTAGACTGGGAAGCCCCAGCCTTCTGCCTCAGGGCTATCTCATT 63 CTTAACACCATCTGGGTAGACTATCAGGAAGCCCCAGCCTTCTGCCTCAGGGCTATCTCATT 64 CAGTACCACCAGCTTAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	:::	325 ProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIleGluVal 344 :: 1188 TCACCTACAGTGGT-TTTCCTGGA	1128 CTCCTGCCCTCAGAGGCCCAGAACGTGACCCTTGTGGCCTACAACAAGCAGGGACCTCT 1187	305 HisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGlyLysSer 324	ProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeuGluLeu	1080 AAGCAGGAC	1021 ACACGTGGTGTCAGAAGAAGCAACTAGATCCAGGGACAGTG-AGTGTGCAGCTGTTCTGG 1079	256	238 GluàlaProCysGlyLeuGluLeuTrpArgValLeuLysProAlaGluàlaAsp 255 ::: 973GCCTGCAGCTGAGGCCTACCATGAAGGGTCCCCCACCATCAGACTGG 1020	937 TCATCTCTGCCTGGATTCTGGAGCCCCTGGAGCCCC972		200 AsnLeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLys 219	180 SerThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyr 199	778 AGTEAGTACATGGAACAGGAGTGTGAACTTCGCTACCAGCCACAGCTCAAAGGAGCCAAC 837	160 ProGluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsn 179	145 ProValLeu	658 CTCGACCCCATGGATGTTGTGAAATTGGAGCCTCCCATGCTGCAGGCCCTGGACATTGGC 717	127 TrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgValLys 144		107 TyrThrileGluValGluAlaGluAenGlyAspGlyValIleLysSerHisMetThrTyr 126	538 GCAAAGAAGAGGCAGAACAACTGCTCCATCCCCCGAAAAAAACTTGCTCCTGTACCAGTAT 597

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                                                                                                                                                                                                                                                                                                   Unpublished contact: Feng Liang Email: fliang@lifetech.com URL: Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                  Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1931)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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HTC; CNSLT_cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Homo sapiens (human).
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            /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                           HisAspLysValGlyGluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSer
                                                                                                                                                                                                                                                                                                                                                                                            LeuAspValAsnThrTrp------MetIleGluTrpPhe-----ProAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---LeuThrGluThrMetAsnThrThrAsnGlnGlnLeuGluLeuHisLeuGlyGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaAspGlyArgArgProValArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluAlaPro---CysGlyLeuGluLeuTrp------ArgValLeuLysProAlaGlu 253
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                  GluIleProLysSerGluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAla
                                                                                            GluGlyProGluThrLysValGluAsnIleGlyValLysThrValThrIleThrTrpLys
                                                                                                                                                                                                                CTGAAGGAGAAC---ATCAGGCCCTTTCAGCTCTATGAGATCATCGTGACTCCCTTGTAC
                                                                                                                                                                                                                                                IleGlnGlnAspLysLeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeu
                                                                                                                                                                                                                                                                                      GCGAGCAATAGCAACAAGACCTGGAGGATGGAACAGAATGGGAGAGCCACGGGTTTCTG
                                                                                                                                                                                                                                                                                                                      ValAspSerGluProThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThr
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CCTGAGCCCCTGAGCTGGGGAAGAGCCCCCCTTACCCACTACACCATCTTCTGGACCAAC
                                                                        CATGCCCCAGAGCTGCATCTAAAGCACATTGGCAAGACCTGGGCACAGCTGGAGTGGGTG
                                                                                                                                          MetGlnAlaCysValAlaGluAsp-----GlnLeuValValLysTrpGlnSerSerAla 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTTCTCAGAAAGCAGAGGCCCAGCTCTGACCAGACTCCAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIleGluVal 344
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                                                                                                                                                                                                                                                                                                                                                                                                                               ------GCCATGGCCCGAGACCCTCACAGCCTCTGGGTAGGCTGGGAGCCCCCC---
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/plasmid="pCMVSPORT_6"
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AUTHORS
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KEYWORDS
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     JOURNAL
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
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Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                    Generation and initial analysis of more than 15,000 full-length
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Mus musculus interleukin 6 signal transducer, mRNA
IMAGE:3598166).
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                                                                                                                                                        human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A.
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Sutheria; Rodentia;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Baylor College of Medicine Human
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLysArgThrTyrAla 73
  IleGlnIleGluTrpIleLysProGluLeuAlaProValSerSerAspLeuLysTyrThr 172
                                                      GTGAAACCCACCCCACCATATAATTTATCAGTGACCAACTCAGAAGAATTATCCAGTATA 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGATAAACCTACAAATTTGACTTGCATTGTGAATGAGGGGAAGAATATGCTGTGCCAG 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
                                                                                                    AlaLysThrGluProProLysIlePheArgValLysProValLeuGlyIleLysArgMet 152
                                                                                                                                                             GCAGAGAATGCCCTTGGGAAGGTCTCCTCAGAGTCTATCAATTTTGACCCCGTGGATAAA 888
                                                                                                                                                                                                         AlaGluAsnGlyAspGlyValIleLysSerHisMetThrTyrTrpArgLeuGluAsnIle 132
                                                                                                                                                                                                                                                                  TGTATGGTCAGCTACATGCCCACCTATTATGTC----AACATTGAAGTCTGGGTGGAA
                                                                                                                                                                                                                                                                                                              CysSerPhe---PheLeuProArgIleThrIleProAspAsnTyrThrIleGluValGlu 112
                                                                                                                                                                                                                                                                                                                                                                       ---ACAGAGAAGTTTCCTGATTGCCAGTCAAAGCATGGCACT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGACCCCGGAAGGGAGACTTACCTTGAAACAAACTACACTTTGAAATCAGAGTGGGCA 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Mammary tumor. C3(1)-Tag model.ductal carcinoma. 5 month old virgin mouse." /clone_lib="NCI_CGAP_Mam6" /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:3598166"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.18e-26
355.00
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29.61%
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Conservative:
Mismatches:
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Gaps:
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90
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774

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Focus

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RESULT 14
CA561173
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AUTHORS
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VERSION
                                                                                                                FEATURES
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                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA561173 592 bp mRNA linear K0283D09-5N NIA Mouse Unfertilized Egg cDNA Library musculus cDNA clone NIA:K0283D09 IMAGE:30052652 5',
                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Other_ESTs: K0283D09-3
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                   Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C..
Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                    Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0283 row: D column: 09
                                                                                                                                                                                                                                       Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                            Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                 (Long)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATCCATGCGAGGAATATAGATCTGTACGGCTCATATGGAAGGCACTGCCTCTT 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysProAlaGluAlaAspGlyArgArgProValArgLeuLeuTrpLysLysAlaArgGly 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaLeuArgCysAlaValLysGluSer-----LysPheTrpSerAspTrpSerGlnGlu 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysAspLysAsnGlnThrTyrAsnLeuThrGlyLeuGlnProPheThrGluTyrValIle 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAAAGCTATCATGGGTCAGTTCAGGGCTGGGCGGTCTT---TTAGATCTAAAGTCTGAC 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgileProAla 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGTCTCACAAACGTACACAGTCACTGGCACAGAGCTGACCGTGAATCTCACCAATGAC 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTAGTGGGACCACATACGAAGACAGACCATCCAAACCACCAAGTTTCTGGTATAAGACA 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysMetGlyMetThrGluGluGluAlaProCys---GlyLeuGluLeuTrpArgValLeu 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGATCCGG---TCCATTAAGGACAGTGGGAAGGGCTACTGGAGTGACTGGAGTGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerPheTrpValSerMetIleSerTyrAsnSerLeuGlyLysSerProValAlaThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeuGluLeuHisLeuGlyGlyGlu 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGAAGCCAATGGGAAAATCTTGGATTATGAAGTG-----ATTCTTACGCAGTCAAAG 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaProValLeuGluLysThrLeuGlyTyrAsnIleTrpTyrTyrProGluSerAsnThr 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGTCTCCTCGAACTTCCTTCACTGTGCAGGACCTCAAGCCTTTTACAGAATATGTGTTTT 1122
                                                                                                                                                       quality sequence stop: 592
                       /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                         Location/Qualifiers
₽
                                                               organism="Mus musculus"
_xref="niaEST:K0283D09-5N"
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Best Local Similarity:
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treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pspORT1 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Unfertilized Egg"
/lab_host="Unfortilized Egg"
/clore 155 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="NIA:K0283D09 I
1.86e-26
347.00
65.89%
51.94%
9.96%
                                                                                                                                                                                                                                                             Yulan Piao (NIA)."
                                                                                                              Length:
Matches:
                             Mismatches:
Indels:
                                                                                   Conservative:
Gaps:
  592
67
18
34
10
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US-10-006-265-2 (1-652) x CA561173 (1-592)
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                                              124
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                                           MetThrTyrTrpArgLeuGluAsnIle 132
                                                                                                                                                                                                                               SerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIle-----
                                                                                                                                                                                                                                                                                                                  TyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThrThrAsnSer 85
                                                                                                                                                                                                                                                                                                                                                                                                       TyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGln 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTGCAAATTCAGCCTGGCAGTCCTGCCGACTAAGCCAGAGAACATTTCCTGCGTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSerCysValTyr 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCCTCTGGGTGTGAACGCTGGAATAATGTGGACCTTGGCACTGTGGGCATTCTCTTTC
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                                                                                                                                                                                                                                                                                TACATTGTGACTTTGACTTACTCCTATGGAAAA-----
                                                                                                                                                                                                                                                                                                                                                                            TACTTCGACAGAAATCTGACTTGCACTTGGAGACCAGAGAAAGGAAACCAATGATACCAGC 408
ATCACATATTGGCATTTAATCTCCATA 591
                                                                                         CCAGACATCTGCAGTGTTGAAGTACAAGCTCAAAATGGAGATGGTAAAGTTAAATCTGAC 564
                                                                                                                                        ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHis 123
                                                                                                                                                                                      AATTATAGTGACAATGCTACAGAGGCTTCATATTCTTTTCCCCCGTTCCTGTGCAATGCCC
                                                                                                                                                                                                                                                                                     ----AGC
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CA560924 479 bp mRNA linear K0279C07-5N NIA Mouse Unfertilized Egg cDNA Library

(Long)

EST 19-NOV-2002

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125 455	109 399	33:	67 299	23:	27 179	11:
ThrTyrTrpArgLeuGluAsnIle 132	105 ABPASnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHisMet 124	87 ThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104	67 ThrvallysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThrThrAsnSerSer 86	47 TyrarglysasnleuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGlnTyr 66 ::: ::	27 CyslyspheSerLeuAlaAlaLeuProAlaLysproGluAsnIleSerCysValTyrTyr 46	119 CCTCTGGGTGTGAACGCTGGAATAATGTGGACCTTGGCACTGTGGGCATTCTCTTTCCTC 178

Search completed: February 23, 2005, 19:23:40 Job time: 6029.32 secs

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Sequence Sequence

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Command line parameters:

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-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XOAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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Match
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Ygapop 10.0 , y
Fgapop 6.0 , F
Delop 6.0 , F
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Novel hemopoletin receptor protein, NR10

Patent: WO 0075314-A 2 14-DEC-2000;

CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU
MAEDA, NORIKO YAGUCHI

OS Homo sapiens (human)

PN WO 0075314-A/2

PD 14-DEC-2000

PF 01-JUN-2000 WO 2000JP003556

PF 02-JUN-1999 JP 99P 155797,30-JUL-1999 JP 99P 217797 PI
MASATSUGU MAEDA,NORIKO YAGUCHI

PC C12N15/12,C12N5/10,C07K14/715,C07K16/28,C12P21/02,G01N33/53,

PC G01N33/566

CC

Location/Qualifiers

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Location/Qualifiers
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Kuijper, J.L.

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Patent: WO 0200721-A 21 03-JAN-2002;
ZymoGenetics, Inc. (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AX365169.1 GI:18696927
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                                                                                                 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg
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AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer
                                                                                                                                                      | IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer
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182 809 142

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368 82 308 62 248 42

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AUTHORS
TITLE
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   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Zhang, W., Wan, T., He, L., Yuan, Z. and Cao, X.

Zhang, W., Wan, T., He, L., Yuan, Z. and Cao, X.

Direct Submission

Submitted (13-NOV-1998) Department of Immunology, Shanghai Brilliance Biotechnology Institute & Second Military Medical University, 800 Xiangyin Road, Shanghai 200433, P.R.China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang,
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Mammalia; Eutheria; Primates;
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hang, W., Wan, T., He,
novel soluble type
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Matches:
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Mismatches:
Indels:
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                                                                                                     AUTHORS
TITLE
JOURNAL
Maeda,M. and Yaguchi,N.

Novel hemopolatin receptor protein, NR10
Patent: WO 0075314 A 14 14-DEC-2000;
CHGGII RESEARCH INSTITUTE FOR MOLECULAR MEDA, NORIKO YAGUCHI
OS Homo sapiens (human)
PN WO 0075314-A/14
PD 14-DEC-2000
PF 01-UN-2000 WO 2000JP003556
PR 02-JUN-1999 JP 99P 155797,30-JUL-1999
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                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
1 (bases 1 to 2119)
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                                                                                                                                                                                                       Novel hemopoietin receptor
BD091877
BD091877.1 GI:22637488
WO 0075314-A/14
Homo sapiens (human)
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JP 99P 155797,30-JUL-1999
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Primates;
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PC C12N15/12,C12N5/10,C07K14/715,C07K16/28,C12P21/02,G01N33/53,
PC G01N33/566
CC CC
FH Key Location/Qualifiers
FT CDS (11)..(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle
                                                                                             PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro
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                                                          SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu
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                                                                                                                                                                                                    GAGTTGGCGCCTGTTTCATCTGATTTAAAATACACACTTCGATTCAGGACAGTCAACAGT
                                                                                                                                                                                                                GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer
                                                                                                                                                                                                                                                                                                       AMATCTCATATGACATACTGGAGATTAGAGAACATAGCGAAAACTGAACCACCTAAGATT
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Sequence 5 from Patent W00229060.
AX467335
AX467335.1 GI:21900585
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hematopoietin receptors hprl and hpr2
Patent: WO 0229060-A 5 11-APR-2002;
Immunex Corporation (US)
Location (Corporation)
                                                                                                                                                                                                                                                                                                                                  LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu
                                                                IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle
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                                       ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAspClnThrTyrAsn
                                                                                                      TTCCGTGTGAAACCAGTTTTGGGCATCAAACGAATGATTCAAATTGAATGGATAAAGCCT
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/db_xref="taxon:9606"
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Patent: WO 0200721-A 68 03-JJ
ZymoGenetics, Inc. (US)
Location/Qualifiers
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                                                       IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu
                                                                                                                              TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn
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                                                                                                                                                                            ATGAAGCTCTCCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTG
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ELAPVSSDLKYTLAFRTYNSTSWMEVNEAKNRKKKNQTYNLTGLQFTEEVIALRCAV
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TCLVKGFYPSDIAVEWSSNGAESSNNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
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_xref="taxon:32630"
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                                                                                US-10-006-265-4 (1-252) x AX467333 (1-2480)
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Best Local Similarity:
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Sequence 3 from E
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AX467333.1 GI:21
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Hematopoietin receptors hpr1 and hpr2
Patent: WO 0229060-A 3 11-APR-2002;
Immunex CorporatioN (US)
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn
                            ATGAAGCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTG 191
                                            MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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Sequence
AX365201
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Patent: WO 0200721-A 53 03-JAN-2002;
ZymoGenetics, Inc. (US)
                                                                                                                                                                                                                                                                                 Sprecher, C.A., and Maurer, M.F
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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ELAPVSSDLKYTLFFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVIALRCAV KESKEWSDWSQEKMGMTEEBAPCGLELMFULKPAEADGRRFVRLLMKKARGAPVLEKT LGYNIMY PESNITULT ETMNITNQQLELHLGGES FWVSMIS IS YNSLGKS PKATIRI FAI QEKSFQCLIEWKQACVAEDQLIVKMOSSALDVNTWMLEWFDVUDSEPTTLSWESVSQAT NWTIQQDKLKPFWCYNISVYPMLHDKVGEPYSIQAYAKEGVPSEGPETKVENIGVKTV TITWKSIFKSEKGIICNYTIFYQAEGGKGFSKTVNSSILQVGLESLKRKTSYIVQVM ASTSAGGTNGTSINFKLSFSVFEIILITSLIGGGLLILIITUTAYGLKKENKLTHLC WPTUPNPAESSISTATWHGDDFKUKLNLKESDDSVNTEDRILKFCSTPSDKLVIDKLVVN FGNVLQEIFTDEARTGQENNLGGEKNGTRILSSCPTSI"

RESULT 9 AY499342 LOCUS DEFINITION Best Local Similarity: Query Match: DB: Alignment Pred. No.: S Ş 밁 δ 밁 δ В S 밁 ঠ 밁 δ 밁 문 S 밁 Ş 문 S 밁 Ś 밁 밁 á US-10-006-265-4 (1-252) x AX365201 (1-2903) Score: Percent Similarity: . . 1157 1097 1037 201 181 977 161 917 141 857 121 797 101 737 677 617 557 497 81 61 41 21 AY499342 2903 bp mRNA linear PRI 10-JUL-2004 Homo sapiens interleukin 31RA splice variant x4 (IL31RA) mRNA, ы GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg ThrSerTyrThrGlnTyrThrValLygArgThrTyrAlaPheGlyGluLygHigAgpAgn TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn ATGAAGCTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTG MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn GAGTTGGCGCCTGTTTCATCTGATTTAAAATACACACTTCGATTCAGGACAGTCAACAGT ANATOTOATATGACATACTGGAGATTAGAGAACATAGCGAAAACTGAACCACCTAAGATT ATAACGATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATT ATTTCCTGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAA TGGATGCTCCCTTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAAC ACCAGCTGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAAAACCAAACGTACAAC 4.6e-120 1292.00 100.00% 100.00% 95.14% Length: Matches: Conservative: Mismatches: Indels: Gaps: 2903 238 0 0 1210 238 1156 1096 1036 40 220 200 160 140 856 100 736 80 676 60 976 120 796 616 556 916 20

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Query Match:
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Eastlake Avenue East, Seattle, WA 98102, USA
Location/Qualifiers
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2 (bases 1 to 2903)
Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M.,
Presnell,S.R., Haugen,H., Bilsborough,J., Maurer,M., Harder,B.,
Johnston,J., Bort,S., Mudri,S., Kuijper,J., Bukowski,T., Shea,P.,
Dong,D., Dasovich,M., Lockwood,L., Levin,S., LeCeil,C., Waggie,K.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2903)

Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J.,

Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J.,

Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,

Harder,B., Johnston,J., Bort,S., Mudij,S., Kuijper,J.L.,

Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,

Lockwood,L., Levin,S.D., LeCiel,C., Waggle,K., Day,H., Topouzis,S.,

Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
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Direct Submission
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MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu
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QEKSFQCIEVMCACVAEDQLVVKWQSSALDVNTWMIEWFPDVDSEPTTLSMESVSVAF
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alternatively spliced"
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497. .2485
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E 1 (bases 1 to 2969)

S Maeda,M. and Yaguchi,N.

Novel hemopoletin receptor protein, NR10

L Patent: WO 0075314-A 1 14-DEC-2000;

CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC
MAEDA, NORIKO YAGUCHI

OS HOMO Sapiens (human)

PN WO 0075314-A/1

PD 14-DEC-2000

PF 01-UTN-2000 WO 2000JP003556

PR 02-UTN-1999 JP 99P 155797,30-JUL-1999 JP 99P

MASATSUGU MAEDA,NORIKO YAGUCHI

PC C12N1-5/12,C12N5/10,C07K14/715,C07K16/28,C12P21/
PC G01N33/566

CC

FH Key Location/Qualifiers
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                               TCAAAGTTCTGGAGTGACTGGAGCCAAGAAAAATGGGAATGACTGAGGAAGAA
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                                                                                                                                             CTCACGGGGCTGCAGCCTTTTACAGAATATGTCATAGCTCTGCGATGTGCGGTCAAGGAG
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Location/Qualifiers
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ratent: WO 0200721-A 17 03-JAN-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ş	3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet	laLeuTrpMet 22	
Дb	129 CTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGG	ACCTGGGCACTGTGGATG 188	
8	23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer	luAsnIleSer 42	
DЬ	189 CTCCCCTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAACATTTCC	AGAACATTTCC 248	
8	43 CysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyL	roGlyLysGluThrSer 62	
Db	249 TGTGTCTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAAACCAGT	AGGAAACCAGT 308	
Q.	63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr	spAsnCysThr 82	
Дb	309 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACA	ATAATTGTACA 368	
δ	83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr	roArgIleThr 102	
9	369 ACCAATAGTTCTACAAGTGAAAATCGTGCTTCGTGCTCTTTTTTTCCTTCC	CAAGAATAACG 428	
Q	103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysS	alileLysSer 122	
Db	429 ATCCCAGATAATTATACCATTGAGGTGGAAAGCTGAAAATGGAGATGGTGTAATTAAATCT	TAATTAAATCT 488	
Qy	123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg	ysIlePheArg 142	
Дb	489 CATATGACATACTGGAGATTAGAGAAAATAGCGAAAAACTGAACCACCTAAGATTTTCCGT	AGATTTTCCGT 548	
δ	143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu	ysProGluLeu 162	
В	549 GTGAAACCAGTTTTTGGGCATCAAACGAATGAATTGAAT	AGCCTGAGTTG 608	
Ş	163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValA	AsnSerThrSer 182	
Дb	609 GCGCCTGTTTCATCTGATTTAAAATACACACTTCGATTCAGGACAGTCAACAGTACCAGC	ACAGTACCAGC 668	

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Submitted (10-DEC-2003) Bioinformatics,
Eastlake Avenue East, Seattle, WA 98102,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H., Bilsborough,J., Maurer,M., Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J., Bukowski,T., Shea,P., Dong,D., Dasovich,M., Lockwood,L., Levin,S., LeCeil,C., Waggie,K., Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kramer, J.,
Gross, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1299)

Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J.,

Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,

Harder,B., Johnston,J., Bort,S., Mudři,S., Kuljper,J.L.,

Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,

Lockwood,L., Levin,S.D., LeCiel,C., Waggie,K., Day,H., Topouzis,S.,

Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
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Homo sapiens interleukin 31RA splice variant
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                                                                           /translation="mmmthalmmlpslckfslaalpakpeniscvyyyrknitctwsp

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/note="class I cytokine
alternatively spliced"
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162. .1136
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Primates;
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USA
                                                                                                                                                                                                     variant
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nt x2 (IL31RA) mRNA,
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SOURCE
ORGANISM
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AY499341
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                                                                                                                                                Homo sapiens interleukin 31RA splice complete cds, alternatively spliced. AY499341 GI:46276460
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1 (bases 1 to 2393)
Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.
Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J.L.,
                                                         Homo sapiens (human)
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2393)
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Gaps:
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Matches:
Conservative:
                                                                                                                                                                                                                     splice variant
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548

488 122 428 102 368 82 308 62

linear PRI 10-555 ht x3 (IL31RA) mRNA,

10-JUL-2004

836 238

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JOURNAL
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2 (bases 1 to 2393)

Dillon, S.R., Sprecher, C., Hammond, A., Rosenfeld-Franklin, M., Billsborough, J., Maurer, M., Harder, B., Presenell, S.R., Haugen, H., Bilsborough, J., Bukowski, T., Shea, P., Johnston, J., Bort, S., Mudri, S., Kuijper, J., Bukowski, T., Shea, P., Johnston, J., Bort, S., Mudri, S., Kuijper, J., Bukowski, T., Shea, P., Johnston, J., Bort, S., LeCeil, C., Waggie, K., Dong, D., Dasovich, M., Lockwood, L., Levin, S., LeCeil, C., Waggie, K., Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parrish-Novak, J. and Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parrish-Novak, J. and
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Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics,
Eastlake Avenue East, Seattle, WA 98102, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Immunol. 5 (7), 752-760 (2004) 15184896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin 31, a cytokine produced by activated T cells, induces dermatitis in mice
                                                                                    LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer
                                                                                                                                                                              CysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="class I cytokine receptor; huzcytor17x3;
alternatively spliced"
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66. .2360
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Cytokine receptor zcytor17
Patent: WO 0200721-A 1 03-JAN-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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Sequence 1 from Patent WO0200721.
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AX365149.1 GI:18696908
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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        Homo sapiens (human)
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RTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPEIPPRKSQYLRSRMPEGTRPE
AKEQLLFSGQSLVPDHLCEEGAPNPYLKNSVTAREFLVSEKLPEHTKGEV"
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Genentech Inc. (US)
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Secreted and transmembrane polypeptides and nucleic a
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                                 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys
                                                                                                  TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr
                                                                                                                                     PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu
                                                                                                                                                                                                      ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu
                                                                                                                                                                                                                                             CATATGACATACTGGAGATTAGAGAACATAGCGAAAACTGAACCACCTAAGATTTTCCGT
                                                                                                                                                                                                                                                          HisMetThrTyrTxpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg
                                                                                                                                                                                                                                                                                                                                                                                                    TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAAACCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet
                                                                                     TGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAAACCAAACGTACAACCTCACG
                                                                                                                                                                                          GTGAAACCAGTTTTGGGCATCAAACGAATGATTCAAATTGAATGGATAAAGCCTGAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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Search completed: February 23, 2005, 15:24:16 Job time: 3193.89 secs

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-QGPG21/USPTO_spool/US1006265/runat 18022005_094657_22172/app_query.fasta_1.2069
-Q=/cgn2_1/USPTO_spool/US1006265/runat 18022005_094657_22172/app_query.fasta_1.2069
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUPFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bite START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORN=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10006265_0GCN_1 1_1098_Grunat_18022005_094657_22172 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Aba93784 Human zcy
Ad126677 Human cyt
Aac92350 Human hae
Aba93821 Human zcy
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ALIGNMENTS

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RESULT 1
AAC92338
ID AAC9
     Maeda M,
                                                                                                                                                                      01-JUN-2000; 2000WO-JP003556
                                                                                                                                                                                                                                                                                                                                                                                           Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10; immunoregulation; haematopoietic cell regulation; transmembrane; immune disorder; haematopoietic disorder; autoimmune disease; allergy;
                                                                                                  02-JUN-1999;
30-JUL-1999;
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                                                                                                                                                                                                                                                                      WO200075314-A1.
                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human haemopoietin receptor protein NR10.2 encoding cDNA SEQ
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                                                  (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Yaguchi N;
                                                                                                  99JP-00155797.
99JP-00217797.
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IJ NO:3.

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hematopoietin receptor protein NR10 for screening potential ligands treatment of immune and hematopoietic disorders such as autoimmune diseases and allergies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    substances for the treatment and prevention of immune and haen disorders including autoimmune diseases and allergies such as
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                                                           ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn
                                                                                                                                GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer
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                                                                               proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders. Agonists or anti-cytor17 antibodies are useful in stimulating cell-mediated immunity for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 the ABA93843 and ABB05730 to ABB05745 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antinflammatory, antiviral, cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2000; 2000US-0214282P
29-JUN-2000; 2000US-0214955P
08-FEB-2001; 2001US-0267963P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polynucleotide useful for treating and spleenic, blood or bone
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P-PSDB; ABB05733.
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                                                            exemplification of the present invention
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antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic
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                       receptor zcytor17 DNA seqid 114.
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Indels:
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Sprecher
Presnell
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14-JUN-2002;
19-DEC-2002;
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GRANT F J.
PRESNELL S R.
WHITMORE T E.
HAMMOND A K.
NOVAK J E.
GROSS J A.
DILLON S R.
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; 2002US-0435361P.
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e TE, Hammond AK, Novak JE,
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                                                                                                                                                                                                                                                                                                                   Dillon SR;
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Novel multimeric or heterodimeric cytokine receptors useful for treating chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, acute inflammatory disease such as endotoxemia, septicemia.

Disclosure; SEQ ID NO 114; 205pp; English

The invention describes an isolated multimeric or heterodimeric cytokine creceptor (I) having at least one polypeptide having 90 percent sequence cidentity with a 732 (S1) or 649 (S2) amino acid sequence given in compeniating residue 20-227 of (S2). (I) is useful for killing cancer cells comprising residue 20-227 of (S1). (I) is useful for killing cancer cells and producing an antibody to (I) and a cytokine-binding domain of a class composition (C1) comprising (I) and a cytokine-binding domain of a class composition (C1) comprising (I) and a cytokine-binding domain of a class composition (C1) comprising (I) and a cytokine-binding domain of a class composition (C1) comprising (I) and a cytokine-composition cells in composition (C1) comprising (I) and a cytokine-composition cells in composition cells and hematopoletic progenitor cells in composition or differentiation composition cells and hematopoletic progenitor cells in cytokine-cytor171ig-induced proliferation or differentiation composition inflammatory disease in which zcytor171ig plays a role. The disease is a composition cells, reducing cytor171ig plays a role. The disease is a composition inflammatory bowel disease is a composition cells, cromn's disease, atopic dermatitis, eczema and cytokine response in a mammal exposed to an antigen or pathogen. An immune response inhibiting composition is useful for inhibiting an inflammatory response in a mammal exposed to an antigen or pathogen. An composition is useful for suppressing an composition in the presence of a composition with other zotror17 receptors in a biological sample. Cc firs acquence encodes a human zotror17 receptors.

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RESULT 4
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ID AAC9
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AC AAC9
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          26-MAR-2001
                                             AAC92350 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUN-1999;
30-JUL-1999;
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                                                                                                                                                                                                                                                                                           Sequence 2119
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P-PSDB; AAB51244.
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encoding CDNA OBS IJ NO:16.

allergy;

Hematopoietin receptor protein NR10 for screening potential ligands treatment of immune and hematopoietic disorders such as autoimmune diseases and allergies.

The present sequence encodes a human haemopoietin receptor protein (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haematopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the identification of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies such as metal and collection of the collection of the substances including autoimmune diseases and allergies such as metal and

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DB:	Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
4.	95.14%	100.00%	100.00%	1292.00	4.98e-134	
Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
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δ	1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
망	11 ATGAAGCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTG 70
8	21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
В	71 TGGATGCTCCCCTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGGCCTGAGAAAC 130
Ş	41 IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
망	131 ATTTCCTGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAA 190
γŞ	61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
망	191 ACCAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAAT 250
Qy	81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
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29-JUN-2000;
08-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                              Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory; antintiammatory; antiviral; antirheumatic; antirthritic; cytostatic; muscular; lymphoid; immune; inflammatory; spleenic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
                                                     Isolated polynucleotide encoding a useful for treating and diagnosing spleenic, blood or bone disorders.
                                                                                                             WPI; 2002-090519/12.
P-PSDB; ABB05743.
The present invention describes a cytokine
                          Example 11; Page 216-221; 235pp; English.
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                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human zcytor17-Fc4 fusion polynucleotide SEQ ID
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SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
                                             LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu
                                                                                  ACCAGCTGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAAACCAAACGTACAAC
                                                                                                        ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn
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                                                                                                                                                                                                                         Alignment
                                                                                                                                                                                                                                                                 Sequence 2295
                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated zcytor17 ligand polypeptide. A polypeptide of the invention has antiinflammatory, dermatological, immunosuppressive, and antimicrobial activity, and may have a use in a vaccine. The polypeptide is useful for treating inflammatory diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's disease, atopic dermatitis, ezzema, psoriasis, endotoxaemia, septicaemia, toxic shock syndrome or infectious diseases. The present sequence is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New zcytor17 ligand polypeptides, useful for treating inflammatory diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn disease, atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia.
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P-PSDB; ADD68180.
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25-APR-2002; 2002US-0375323P
19-DEC-2002; 2002US-0435315P
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                                                                 Homo sapiens
                                                                                                                             Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia; septicaemia; toxic shock syndrome; zcytor17lig; zcytor17; Fc4;
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MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu

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ATTTCCTGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAA

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TGGATGCTCCCTTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAAC

MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu

ATGAAGCTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTG

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The invention describes an isolated multimeric or heterodimeric cytokine receptor (I) having at least one polypeptide having 90 percent sequence CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in Specification, and where (I) binds a ligand comprising a 164 (S3) amino CC acid sequence, given in specification, or at least one polypeptide CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells CC and producing an antibody to (I) and a cytokine-binding domain of a class CC binding domain of a class I cytokine-binding domain of a class CC binding domain of a class I cytokine receptor and a vehicle is useful for reducing haematopoietic cells and hematopoietic progenitor cells in a mammal; inhibiting zcytor171ig-induced proliferation or differentiation CC inflammatory disease in which zcytor171ig amammal afflicted with an inflammatory disease in which zcytor171ig pays a role. The disease, CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and CC underative colitis, Crohn's disease, atopic dermatitis, eczema and CC phoriasis. The disease is acute inflammatory disease such as inflammatory disease such as cimune response inhibiting composition is useful for inhibiting an inflammatory response inhibiting composition is useful for suppressing an inflammatory response inhibiting composition is useful for suppressing an inflammatory response in a mammal exposed to an antigen or pathogen. An outlinearic or heterodimeric cytokine receptor in a biological sample. This sequence encodes a soluble human zcytor17-human Fc4 (not defined)
Sprecher
Presnell
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14-JUN-2002;
19-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel multimeric or heterodimeric cytokine receptors useful for treating chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, acute inflammatory disease such as endotoxemia,
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(HAMM/)
(NOVA/)
(GROS/)
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(KUIJ/)
(DASO/)
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DB; ADL26603.
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DASOVICH M M.
GRANT F J.
PRESNELL S R.
WHITMORE T E.
HAMMOND A K.
NOVAK J E.
GROSS J A.
GROSS J A.
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2002US-0435361P.
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Whitmore
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re TE, Hammond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grant FJ;
E, Gross
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Percent Similarity:
Best Local Similarity:
Query Match:

5.6e-134 1292.00 100.00% 100.00% 95.14%

Length:
Matches:
Conservative: Mismatches: Indels:

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Homo sapiens

Location/Qualifiers

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                                                                                                                                         Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation; pancytopaenia; leukopaenia; anaemia; thrombocytopaenia; osteoporosis; neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder; cancer; myelodysplastic syndrome; idiopathic thrombocytopaenic purpura; ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia; osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy; anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease; demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome; vertebral disc disease; myasthenia gravis; chronic neuronal degeneration; stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD38772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human haematopoietin receptor 1 (HPR1) cDNA.
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The present invention relates to human and murine haematopoietin receptor CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for treating cell proliferation conditions e.g., pancytopaenia, leukopaenia, CC anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis CC resulting from a lack of bone-forming cells. They are also useful for treating cell proliferation conditions such as leukaemia and tumour CC metastasis, osteoporosis resulting from an excess of bone-resorbing CC diseases such as cell proliferation, metabolic and reproductive hormone CC diseases such as cell proliferation, metabolic and reproductive hormone CC diseases such as cell proliferation, metabolic and reproductive hormone CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, CC carcinoma, carcinoma (e.g., adenocarcinoma (E.g., osteosarcoma, sarcoma), carcinoma (e.g., adenocarcinoma (E.g., osteosarcoma, concer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia cod displastic syndromes (including refractory anaemia, refractory anaemia, color purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
CC myeloid metaplasia, osteoclast disorders that lead to bone loss such as cortactory including content of the monocrotaci including content cancer should be propored to content the content of the co
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13-OCT-2000; 2000US-0240476P
20-FEB-2001; 2001US-0270282P
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osteoporosis including post-menopausal osteoporosis,
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                                                                                                                                                                                                                            CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, CC antixheumatic, antiarthritic and muscular activities. The zcytor17 CC proteins are useful for treating and diagnosing lymphoid, immune, CC inflammatory, spleenic, blood or bone disorders. Agonists or anti-ccytor17 antibodies are useful in stimulating cell-mediated immunety and CC for stimulating lymphocyte proliferation, such as in the treatment of cifections involving immunosuppression, including certain viral CC infections. They are also useful for inducting cytotoxicity and for creating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatorid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to Chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the CX exemplification of the present invention
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29-JUN-2000;
08-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polynucleotide encoding a cytokine receptor zyctor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders.
                                                                                                                                                                                                        Sequence 2903
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21-JAN-2003; 2003WO-US001984.
                                                                                                                                                                                                                                                                                Human zcytor17 cDNA SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                             15-JAN-2004
                                                                                                                                                                                                                                                                                                                                          ADD68146;
                                                                                                                                                                                          immunosuppressive; antimicrobial; vaccine; inflammatory disease; inflammatory bowel disease; ulcerative colitis; Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia; septicaemia; toxic shock syndrome; infectious disease.
                                                                                                                                                                                                                                                   ss; gene; human; zcytor17; antiinflammatory;
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                                                                                                                Location/Qualifiers
                                                                                       /product= "zcytor17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel isolated zcytor17 ligand polypeptide. A polypeptide of the invention has antiinflammatory, dermatological, immunosuppressive, and antimicrobial activity, and may have a use in a vaccine. The polypeptide is useful for treating inflammatory diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicaemia, toxic shock syndrome or infectious diseases. The present sequence is used in
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25-APR-2002; 2002US-0375323P.
19-DEC-2002; 2002US-0435315P.
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GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer
                                         PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro
                                                                                       LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle
                                                                                                                          ATAACGATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATT
                                                                                                                                        IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyVallle
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14-JUN-2002; 2002US-0389108P.
19-DEC-2002; 2002US-0435361P.
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PRESNELL S R.
WHITMORE T E.
HAMMOND A K.
NOVAK J E.
GROSS J A.
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d AK, Novak JE,
                                                                                                                                                                                                                                                                                   Grant FJ;
                                                                                                                                                                                                                                                             Gross
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Novel multimeric or heterodimeric cytokine receptors useful for chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, acute inflammatory disease such as endotoxen

disease such as endotoxemia,

Example 3;

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-006-265-4 (1-252) x ADL26569
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GAGTTGGCGCCTGTTTCATCTGATTTAAAATACACACTTCGATTCAGGACAGTCAACAGT
                          GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer
                                                                                                                                PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro
                                                                                                                                                                                                                                 Ly6SerH18MetThrTyrTrpArgLeuGluAsnIleAlaLy8ThrGluProProLysIle
                                                                                                                                                                                                                                                                                                                                       | IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle
                                                                                                                                                                                                                                                                                                                                                                                                                                          CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn
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                                                                                                                                                                                                      ANATCTCATATGACATACTGGAGATTAGAGAAACATAGCGAAAACTGAACCACCTAAGATT
                                                                                                                                                                                                                                                                                                         ATAACGATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATT
                                                                                                                                                                                                                                                                                                                                                                                                               ACCAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAAT
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Matches:
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Best Local Similarity:
Query Match:

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                                                                                                                The present sequence encodes a human haemopoietin receptor protein (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haematopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the identification of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies such as metal and called a light of the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 200
P-PSDB;
    Sequence 2969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hematopoietin receptor protein NR10 for screening potential ligands for treatment of immune and hematopoietic disorders such as autoimmune diseases and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-1999;
30-JUL-1999;
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                                                                                          pollen allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 3-5; 127pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2000; 2000WO-JP003556
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DB; AAB51242.
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99JP-00217797.
    939 A;
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                                                                                                                                                        Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory; antiviral; antirheumatic; antiviral; cytostatic; muscular; lymphoid; immune; inflammatory; spleenic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
                                                                                                                                                                                                                                                                                                        01-MAY-2002
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   26-JUN-2001; 2001WO-US020484.
                                      03-JAN-2002
                                                                       WO200200721-A2
                                                                                                                                                                                                                                                                  Zcytor17 soluble form truncated in the fibronectin domain cDNA SEQ:17.
                                                                                                                                           inflammatory disease; pancreatitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a cytokine receptor designated zcytor17. CC Zcytor17 has immunomodulatory, antiinflammatory, antivital, cytostatic, cantirheumatic, antiarthritic and muscular activities. The zcytor17 cc antirheumatic, antiarthritic and muscular activities. The zcytor17 cc proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders. Agonists or anticzytor17 antibodies are useful in stimulating cell-mediated immunity and crytor17 antibodies are useful in stimulating cell-mediated immunity and crytor17 antibodies are useful in the treatment of infections involving immunosuppression, including certain viral crimetrions. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, cpancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the
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29-JUN-2000; 2000US-0214955P.
08-FEB-2001; 2001US-0267963P.
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 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg
                                                          IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
                                                                                                                                                                                                TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr
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                                                                                                                          ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
                                                                                                                                                                               TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACA
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                                                                       Sprecher Presnell
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                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2002; 2002US-0350325P.
14-JUN-2002; 2002US-0389108P.
19-DEC-2002; 2002US-0435361P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disease; inflammatory bowel disease; ulcerative colitis; Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia; septicaemia; toxic shock syndrome; zcytor17; human; gene; ss.
WPI; 2003-876545/81.
P-PSDB; ADL26676.
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DASOVICH M M.
GRANT F J.
PRESNELL S R.
WHITMORE T E.
HAMMOND A K.
NOVAK J E.
GROSS J A.
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Novel multimeric or heterodimeric cytokine receptors useful for treating chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, acute inflammatory disease such as endotoxemia,

Disclosure; SEQ ID NO 112; 205pp; English

CC receptor (I) having at least one polypeptide having 90 percent sequence CC identity with a 732 (SI) or 649 (S2) amino acid sequence given in Specification, and where (I) binds a ligand comprising a 164 (S3) amino CC acid sequence, given in specification, or at least one polypeptide comprising residue 20-227 of (SI). (I) is useful for killing cancer cells CC and producing an antibody to (I) and a cytokine-binding domain of a class I cytokine receptor. A composition (CI) comprising (I) and a cytokine-binding domain of a class I cytokine receptor and a vehicle is useful for: reducing haematopoietic cells and hematopoietic progenitor cells in CC a mammal; inhibiting zcytor1711g-induced proliferation or differentiation confident of inflammatory disease in which zcytor171ig plays a role. The disease is a chronic inflammatory disease such as inflammatory bowel disease is a chronic inflammatory disease, atopic dematities, eczema and CC endotoxaemia, septicaemia, toxic shock syndrome and infectious disease. An immune response in hibiting composition is useful for suppressing an imflammatory response in a mammal exposed to an antigen or pathogen. An imflammatory response in a mammal axion inflammation. An antibody that composition by the presence of a comprisically binds to (I) is useful for detecting the presence of a comprisically binds to (I) is useful for detecting the presence of a comparison with other receptor in a biological sample. The invention describes comparison with other zcytor17 receptors. an isolated multimeric or heterodimeric cytokine

Sequence 1299 BP; 402 A; 276 C; 306 G; 315 T; 0 U; 0 Other;

US-10-006-265-4 (1-252) x ADL26675 (1-1299)

142	123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142	Ś
488	429 ATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATTAAATCT 4	В
122	103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 1	Ś
428	369 ACCAATAGTTCTACAAGTGAAAATCGTGCTTCGTGCTCTTTTTTTCCTTCC	밁
102	83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr :	8
368	309 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACA	망
82	63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr	Ś
308	249 TGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAAACCAGT	망
62		ફ
248	189 CTCCCCTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAACATTTCC	망
42	23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42	Ş
188	129 CTCTCTCCCCAGCCTTCATGTGTTTAACCTGGGGATGTTGGACCTGGGCACTGTGGATG	뮍
22	3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22	δ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory; antiinflammatory; antiviral; antirheumatic; antiarchritic; cytostatic; muscular; lymphoid; immune; inflammatory; spleenic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders Agonists or antizcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral
                                                                                                                                                                                                                                                                                               Isolated polynucleotide encoding a useful for treating and diagnosing spleenic, blood or bone disorders.
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29-JUN-2000; 2000US-0214955P.
08-FEB-2001; 2001US-0267963P.
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                                                  GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys
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            PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu
                                                                                                                     TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr
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Search completed: February 23, 2005, 09:54:14
Job time: 382.207 secs

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Result
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-MODEL-Frame+ p2n.model -DEV=xlh
-Q-/cgn2 1/USPTO_spool/US1006265/runat 18022005_094658_22207/app_query.fasta_1.2069
-Q-/cgn2 1/USPTO_spool/US10006265/runat 18022005_094658_22207/app_query.fasta_1.2069
-DB=18sued_Patents_NA -QFMT=fastap_SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS_Site START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODEL-COAL -OUTENT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10006265_0CGN 1 1_143 @runat 1802205_094658_22207 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-825-558-3
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APPLICANT:	Ä		Masayuki	Έ.			
APPLICANT:		Ohtomo.	Toshihiko	6			
TITLE OF	Ħ		NOVEL METHOD	EIH	OD FOR GENE CLONING		
FILE RE	FERENCI	REFERENCE: 06501-070001	1-07000	:	3		
CORRENT	APPLIA	APPLICATION NUMBER:	NOMBER:	2 6	709/700,8200		
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	FILING DATE.	- 2		2 5	7/0/201		

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NESULT 1 US-09-700-820C-17 Sequence 17, Application US/09700820C Patent No. 6610485 GENERAL INFORMATION. APPLICANT: Saito, Mikiyoshi APPLICANT: Saito, Mikiyoshi APPLICANT: Saito, Mikiyoshi APPLICANT: Saito, Mikiyoshi APPLICANT: Ohtomo, Toshihiko TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING FILE REFERENCE: 06501-070001 CURRENT FILING DATE: 2000-11-20 PRIOR APPLICATION NUMBER: US/09/700,820C CURRENT FILING DATE: 1998-04-30 PRIOR APPLICATION NUMBER: JP 10/138652 PRIOR APPLICATION NUMBER: JP 10/138652 PRIOR FILING DATE: 1998-05-20 PRIOR FILING DATE: 1998-05-20 PRIOR FILING DATE: 1998-10-01 NUMBER OF SEQ ID NOS: 39 SEQ ID NO 17 LENGTH: 2995 TYPE: DNA ORGANISM: Mus musculus FEATURE: NAME/KEY: CDS INCATION: (29)...(2839) US-09-700-820C-17 Alignment Scores: Pred. No.: Score: Score: Score: Score: Score: Secore: Sec

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US-08-825-558-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08825558
Patent No. 5965724
GENERAL INFORMATION:
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              APPLICANT: SHĀRKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                       STATE:
                                     APPLICATION NUMBER: US/08/825,558 FILING DATE: 19-MAR-1997
                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153
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                                                                                                                                                                                                           20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCAATATAGGACCAAAGATGCCTCAACTTGGATCCAGGTCCCTCTT---GAAGATACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysMetGlyMetThrGluGluGlu 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTAAAGCTATCATGGGTCAGTTCAGGGCTGGGCGGTCTT---TTAGATCTAAAGTCTGAC 856
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
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REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA FEATURE:
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LENGTH: 1977 base pairs
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STRANDEDNESS: both
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                                                        PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
                                                                                                                                                                                                                                                                                                                             ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
                                                                                                                                                                                                                                                                                                                                                                                ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrTyrAlaPheGlyGlu------LysHisAsp-----AsnCysThrThrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGATGGTGGAAGGAAACACACTTGGAGACAACTTCACTTTAAAATCTGAATGGGCA 495
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                                       TACTGGAGTGACTGGAGTGAAGAAGCAAGTGGGATCACCTATGAAGAT
                                                                                                                                                  LeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGluSerLys---
                                                                                                                                                                                                         AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAGAC
                                                                                                                                                                                                                                                   MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly
                                                                                                                                                                                                                                                                                            AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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PATENT NO. 6380160
GENERAL INFORMATION:
APPLICANT: SHAKKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2023)71-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,611
FILING DATE: 17-MAY-1999
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ZIP: 20005
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                                 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
                                                                                                                                                                                     71 ThrTyrAlaPheGlyGlu------LysHisAsp-----AsnCysThrThrAsn 84
                                                                                                                                                                                                                                                             55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg
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                                                                                                           SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
                                                                                                                                                  ACACACAAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT
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262.50
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Indels:
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Matches:
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RESULT 4
US-07-797-556-1
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NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELECHONE: 206-587-0430
TELECAX: 206-587-0666
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Gearin
                             ORIGINAL SOURCE:
TISSUE TYPE: hu
IMMEDIATE SOURCE:
CLONE: B10G/pDC
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APPLICATION NUMBER: US
FILING DATE: 19911122
CLASSIFICATION: 435
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
           FEATURE:
                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                         FRAGMENT TYPE:
                                                                                                                        ANTI-SENSE: NO
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CITY: Seattle
NAME/KEY:
                                                                                                                                                                                                         TYPE: NUCLEIC ACID
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925 TACTGGAGTGACTGGAGTGAAGAAGCAAGTGGGATCACCTATGAAGAT 972
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                                 B10G/pDC303
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Receptor for Oncostatin M and Leukemia
Inhibitory Factor
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RESULT 5
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Best Local Similarity:
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                                                                                   Sequence 1, Application US/08308881 Patent No. 5783672 GENERAL INFORMATION:
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FEATURE:
NAME/KEY:
LOCATION:
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FEATURE:
NAME/KEY:
                APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              1168 TACTGGAGTGACTGGAGTGAAGAAGCAAGTGGGATCACCTATGAAGAT 1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                             164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
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Percent Similarity:
Best Local Similarity:
Query Match:
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TELEX: 756822
INFORMATION FOR SEQ ID NO:
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FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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LENGTH: 2369 base pairs
TYPE: nucleic acid
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FILING DATE: 12-SEP-:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                        No.:
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LOCATION:
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                                                            TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg
                            ThrTyrAlaPheGlyGlu------LysHisAsp-----AsnCysThrThrAsn 84
ACACACAAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT 798
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Matches:
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Indels:
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RESULT 6
US-09-058-263-1
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Patent No. 5891997
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (200) 587-0430
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk COMPUTER: Apple Macintosh OPERATING SYSTEM: Apple 7.1 SOFTWARE: Microsoft Word, Version CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/058,263
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MEDIUM TYPE: Floppy
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                                                                 TELEPHONE: (200) 233-0644
                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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TISSUE TYPE: human |
IMMEDIATE SOURCE:
CLONE: B10G/pDC303
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
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                                                                                                                                                        184
                                                                                                                                                                                            994
                                                                                                                                                                                                                                                                934 ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                    105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyVallleLysSer---His 123
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                                                                                                                                                                                                                                                                                                                                                                      124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
                                                                                                                                                                                                                                                                                                                                                                                                             820 ---AACATTGAAGTCTGGGTAGAAAGCAGAGAATGCCCTTGGGAAGGTTACATCAGATCAT
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                                                                                                                                                    MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
         PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
                                             LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
                                                                                                                                                                                        AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
                                                                                                                                                                                                                          ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro
                                                                                                                                                                                                                                                                                                                                        ATCAATTTTGATCCTGTATATAAAGTG----AAGCCCAATCCGCCACATAATTTATCAGTG
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Matches:
Conservative:
Mismatches:
Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                  US-09-059-099-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
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                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
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APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
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SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
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APPLICATION NUMBER:
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                                                                                 No.:
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STREET: 51
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COUNTRY:
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OPERATING SYSTEM: Apple 7
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Mismatches:
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                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
   PRIOR APPLICATION DATA:
               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                          STREET: 51 Und
                                                APPLICATION NUMBER:
                                                                                                                                                                            COUNTRY:
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51 University Street
                                                                                                                                                                              USA
                                                US/09/058,264
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APPLICATION NUMBER: US/0 FILING DATE: 12-SEP-1994

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FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECHMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: TISSUE TYPE: human placenta
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             144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
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                                                                                                                                                                                                       85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
                                                                                                                                                                                                                                                                    71 ThrTyrAlaPheGlyGlu------LysHisAsp------AsnCysThrThrAsn 84
                                              ATCAATTTTGATCCTGTATAAAGTG---AAGCCCAATCCGCCACATAATTTATCAGTG
                                                                           MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
                                                                                                                                                                          TATTCTACT------GTGTATTTTGTC------
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                                                                                                                                                                                                                                                                                                                             TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg 70
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YPE: N-terminal
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244..309
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51.85%
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19.33%
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Matches:
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Indels:
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US-09-455-962-1
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                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/058,26
PILING DATE: US 08/249
PILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98101
ZIP: 98101
COMPUTER READABLE FORM:
Floppy disk
                                                  IMMEDIATE SOURCE:
CLONE: B10G/pD
                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Receptor for NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                            TELEFAX: 156822
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OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version
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                NAME/KEY:
                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/455,962
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Best Local Similarity:
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           Sequence 1, Application PC/TUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex.Corporation
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1168 TACTGGAGTGACTGGAGTGAAGAAGCAAGTGGGATCACCTATGAAGAT 1215
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51 University Street
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Mismatches:
Indels:
Gaps:
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TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08,
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE: N-
ORIGINAL SOURCE:
TISSUE TYPE: h
IMMEDIATE SOURCE:
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
LENGTH: 2369 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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LOCATION:
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                                                                                                     TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg
               ACACACAAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT 798
                                           ThrTyrAlaPheGlyGlu------LysHisAsp-----AsnCysThrThrAsn 84
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YPE: N-terminal
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Matches:
Conservative:
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Indels:
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US-08-825-558-5
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                                                                                                                                                                                                         SOFTWARE: PATENTIN Release #1.0, Ve. CURRENT APPLICATION NUMBER: US/08/825,558 FILING DATE: 19-MAR-1997 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: ESMOND, ROBERT W. REGISTRATION NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 0623.05300 TELECOMMUNICATION INFORMATION:
                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: STERNE, KESSLER, (
STREET: 1100 NEW YORK AVENUE
                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                              TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 NEW CITY: WASHINGTON
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
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                                                                                                                                                                                                               Sequence 5, Application US/09312611 Patent No. 6380160 GENERAL INFORMATION:
STREET: 1100 ... CITY: WASHINGTON CTATE: DC
                                                                                                                         APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
APPLICANT: DELLOW, GD130 Lacking
                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Matches:
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Best Local Similari
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,611
FILING DATE: 17-MAY-1999
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)371-254
INFORMATION FOR SEQ ID NO:
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NAME/KEY:
LOCATION:
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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
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MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
                                         AGTGTTATAATA----CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
                                                                            ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
                                                                                                                                                                                                                                                                                                                                                                                                    SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
                                                                                                                                                                                                                                                                                 ---AACATTGAAGTCTGGGTAGAAGCAGAGAATGCCCTTGGGAAGGTTACATCAGATCAT
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Indels:
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                                                                                                                                                                                              US-10-006-265-4 (1-252) x US-08-795-473B-4 (1-3085)
                                                                                                                                                                                                                                                                                                          score:
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                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                       Percent Similarity:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)-997-103
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32.7
REFERENCE/DOCKET NUMBER: 963.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: A Pharmaceutical Composition for Treating TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3085 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
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ThrTyrAlaPheGlyGlu------LysHisAsp------AsnCysThrThrAsn 84
                                                                      TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg
                                                                                                                                                         ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
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                                                     TGGGATGGTGGAAGGGAAACACACTTGGAGACAAACTTCACTTTAAAATCTGAATGGGCA 750
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1140 Avenue of the Americas
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Nahot, Orit
Blum, Herbert E.
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Conservative:
Mismatches:
Indels:
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Sequence 4, Application US/094398:
Patent No. 6410009
GENERAL INFORMATION:
APPLICANT: Galun, Eithan
APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/795,473
FILING DATE: 11-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPAN: (212)-997-1028
TELEPAN: (212)-997-1037
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-439-856-4
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: A Pharmaceutical Composition for Treating TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1140 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
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US-09-023-655-1131
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Best Local Similarity:
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                                                                                                                                                                      Sequence 1131, Application US/09023655
Patent No. 6607879
                                                      GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
                     NUMBER OF SEQUENCES: 1
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     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAATTTTGATCCTGTATATAAAGTG----AAGCCCCAATCCGCCACATAATTTATCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro
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                                                                                                                                                                                                                                                                                                                                            TGGGATGGTGGAAGGGAAACACACTTGGAGACAAACTTCACTTTAAAATCTGAATGGGCA
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   INCYTE PHARMACEUTICALS,
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1131:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: FC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORD PERFECT 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: GENBAI
CLONE: 9186353
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STRANDEDNESS: sing
                                   889 ATCAATTTTGATCCTGTATATAAAGTG---AAGCCCAATCCGCCACATAATTTATCAGTG
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144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
                                                                                                                                                    105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His
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                                                                                                                                                                                                                                                                                                                                                                       55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                              35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr
                                                                                                                                                                                                                               85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
                                                                                                                                                                                                                                                                                                          71 ThrTyrAlaPheGlyGlu------LysHisAsp-----AsnCysThrThrAsn
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CALIFORNIA
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                                                                       MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal
                                                                                                                  --- AACATTGAAGTCTGGGTAGAAGCAGAGAATGCCCCTTGGGAAGGTTACATCAGATCAT
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Mismatches:
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                                LeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGluSerLys---
                                                              AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAGAC 1119
                                                                             MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly
                                                                               203
                                                                                             1062
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Search completed: February 23, 2005, 19:36:05

Job time : 126.023 secs

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Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -MODEL-Frame+ D21.model -DEV=xlh
-MODEL-Frame+ D21.model -DEV=xlh
-Q-(cgn2 1/USPTO_spool/US10006265/runat_18022005_094659_22236/app_query.fasta_1.2069
-Q-(cgn2 1/USPTO_spool/US10006265/runat_18022005_094659_22236/app_query.fasta_1.2069
-Q-(cgn2 1/USPTO_spool/US10006265 -START=1 -END=-1 -MATRIX=blosum62
-LOOPEX=0 -LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -OCCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER-US1006265 @CGN 1 1 1175 @TUNAT_18022005_094659_22236
-NCPU=6 -ICPU=3 -NO_MAAP -LARCEQUERY -NEG SCORES=0 -MATT_DSBELOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB seq length: 0
DB seq length: 2000000000
                                                                                                                                                                          Published_Applications_NA:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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/Cgn2_6/ptcdata/1/pubpna/USO7_PUBCOMB.seq:*
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/Cgn2_6/ptcdata/1/pubpna/USO8_PUBCOMB.seq:*
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/Cgn2_6/ptcdata/1/pubpna/USO9_PUBCOMB.seq:*
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/Cgn2_6/ptcdata/1/pubpna/USO9_PUBCOMB.seq:*
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/Cgn2_6/ptcdata/1/pubpna/USO9_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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3796.488 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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32-233-9	S-10-232-23	S-10-230-260-9	-10-219-481-	6-6/8-6TZ-0T-	S-10-219-456	100 010 100 100	-10-219-464-9	-10-219-075-	-10-219-003-	-10-230-434-	19-076-	27-883-	-10-227-873-	-10-218-84	-10-216-159A-	-10-232-224-9	-10-230-414-9	-10-218-63	-10-230-338-9	-10-230-16	-10-227-884-	-10-772-531-	-10-351-157-	-09-892-949-1	-10-772-531-	-10-351-157	-09-892-949-	-10-006-265-1	-10-772-531-	-10-352-554-	-10-351-157-	-09-892-949-	-10-715-66	-09-972-708-	-10-772-531-6	-10-352-554-3	-10-351-157-	-09-892-949-6	-10-715-667-	S-09-972-708-	-10-006-265-1	-531-2	-10-351-157-1	US-09-892-949-21	-10-006-265-		ID	
e 91, App	, T.	ddw 'Te	91, App	לחפזורם אדי אלה	equence 91,	equence of the	emience 91. App	emience 91 App	equence 91, App	ဓို	equence 91,	equence 91,	1,	equence 91,	equence 91,	equence 91,	equence 91,	equence	equence 91,	equence 91,	equence 91	equence 1,	equence 11	equence 1,	equence 17	equence 11	equence 17, App	equence 1,	equence 53, App	equence 4,	equence 4, Appl	equence 53,	equence 3,	equence 3, 1	equence 68,	equence 38	equence 38, App	equence 68,	equence 5, Appl	equence 5,	e 16, App	e 21,	Sequence 114, App	Sequence 21, Appl	equence 3, Appl	1 (1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Description	

ALIGNMENTS

RESULT 1 US-10-006-265-3

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Sequence 3, Application US/10006265
publication No. US20030125520A1
GENERAL INFORMATION:
APPLICANT: Maeda, Masatsugu
APPLICANT: Yaguchi, No. US20030125520A1iko
ITITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001
CURRENT APPLICATION NUMBER: US/10/006,265
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/JP00/03556
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR APPLICATION NUMBER: JP 11/15797
PRIOR PRILING DATE: 1999-06-02
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 40
SOPTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity:
            RESULT 2
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 Sequence 21,
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (523)...(1278)
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                                                                                                   TCAAAGTTCTGGAGTGACTGGAGCCAAGAAAAATGGGAATGACTGAGGAAGAAGGCAAG
                                                                                                               SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluGlyLys
                                                                                                                                                                                                ACCAGCTGGATGGAAGTCAACTTCGCTAAGGAACCGTAAGGATAAAAAACCAAACGTACAAC
                                                                                                                                                                                                            ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn
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  Application US/09892949
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GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR APPLICATION NUMBER: US 60/27,963
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 1476
TYPE: DNA
OPCANION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens FEATURE: AMME/KEY: CDS ; LOCATION: (162)...(878) US-09-892-949-21
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             163
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                                                 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu
                                                                                     HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg
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                                                                                                                                     ATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATTAAATCT
                                                                                                                                                   IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer
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                                      GTGAAACCAGTTTTGGGCATCAAACGAATGATTCAAATTGAATGGATAAAGCCTGAGTTG
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1343.00
99.60%
99.60%
98.90%
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Gross, Jane A.

APPLICANT: Dillon, Stacey R.

FILE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MUL-
FILE REFERENCE: 02-02

CURRENT APPLICATION NUMBER: US/10/351,157

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US 60/435,361

PRIOR FILING DATE: 2002-12-19

PRIOR FILING DATE: 2002-06-14

PRIOR APPLICATION NUMBER: US 60/389,108

PRIOR APPLICATION NUMBER: US 60/350,325

PRIOR APPLICATION NUMBER: US 60/350,325

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 183

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 114

LENGTH: 1476

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

LOCATION: (162)...(878)

US-10-351-157-114
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Publication No. US20030215838A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Coseph L.
APPLICANT: Kuljper, Joseph L.
APPLICANT: Dasovich, Maria M.
APPLICANT: Dasovich, Maria M.
APPLICANT: Dresnell Scott R.
APPLICANT: Whitmore, Theodore
APPLICANT: Hammond, Angela K.
APPLICANT: No. US20030215838A1
APPLICANT: Gross, Jane A.
APPLICANT: Gross, Jane A.
APPLICANT: Gross, Jane A.
APPLICANT: Dillon, Stacey R.
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Best Local Similarity:
Query Match:
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US-10-351-157-114
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Dasovich, Maria M.
Grant, Francis J.
Presnell, Scott R.
Whitmore, Theodore E.
Hammond, Angela K.
No. US20030215838Alak, Julia E.
                                                   LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
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                                                                                                        CTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTGTGGATG 188
                                                                                                                             LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet
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1343.00
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Matches:
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                                                                                                                  Sequence 21. Application US/10772531

Publication No. US2004014242A1

GENERAL INFORMATION:

APPLICANT: Spreecher, Cindy A.

APPLICANT: Presnell, Scott R.

APPLICANT: Presnell, Scott R.

APPLICANT: Maider, Joseph L.

APPLICANT: Maider, Mark F.

TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17

FILE REFERENCE: 00-42

CURRENT FILING DATE: 2004-02-05

PRIOR APPLICATION NUMBER: US/10/772,531

CURRENT FILING DATE: 2001-06-26

PRIOR APPLICATION NUMBER: US 60/214,282

PRIOR FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: US 60/214,955

PRIOR APPLICATION NUMBER: US 60/214,955

PRIOR APPLICATION NUMBER: US 60/214,955

PRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/267,963

PRIOR FILING DATE: 2001-08-09

PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Wind
SEQ ID NO 21
LENGTH: 1476
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-772-531-21
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Percent Similarity:
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Query Match:
DB:
RESULT 5
US-10-006-265-16
; Sequence 16, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
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; NAME/KEY: CDS
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APPLICANT: Yaguchi, No. US20030125520A1iko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PRO
FILE REFERENCE: 06501-096001
CURRENT APPLICATION NUMBER: US/10/006,265
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCIJP00/03556
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR APPLICATION NUMBER: JP 11/15797
PRIOR PILING DATE: 1999-06-02
PRIOR FILING DATE: 1999-06-02
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 2119
TYPE: DNA
OCCANATION UNA
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LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCy8AlaValLysGlu
                                                              ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn
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APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Mosley, Steven R.
APPLICANT: Bird, Timothy A.
APPLICANT: DuBose, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 ANI
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/09/972,708
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
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LENGTH: 2238
TYPE: DNA
ORGANISM: Homo sapiens
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GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
                                                    PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
                                                                                                                       Ly8SerHisMetThrTyrTrpArgLeuGluAsnIleAlaLy8ThrGluProProLy8Ile 140
                                                                                                                                                                  ATAACGATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGAATT
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                                   TGGATGCTCCCTTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAAC
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GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Cosman, David J.

APPLICANT: Mosley, Bruce A.

APPLICANT: Bird, Timothy A.

APPLICANT: DiBose, Robert F.

APPLICANT: DiBose, Robert F.

APPLICANT: Wiley, Steven R.

TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2

FILE REFERENCE: 3160-B

CURRENT APPLICATION NUMBER: US/10/715,667

CURRENT FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: US/09/972,708

PRIOR APPLICATION DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.1

SEQ ID NOS
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TYPE: DNA
ORGANISM: Homo sapiens
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   ATAACGATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATT
                   IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
                                                                                                                                 ACCAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAAT
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APPLICANT: Sprecher, Cindy A.
APPLICANT: Presmell, Scott R.
APPLICANT: Gao, Zeren
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
RUMBER OF SEQ ID NOS: 93
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APPLICANT: Kuijper, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2295
TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION: Polynucleitide encoding human zcytor17-Fc4
NAME/KEY: CDS
LOCATION: (1)...(2295)
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                                                            MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu
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       TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn
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APPLICANT: DIIION, Stacey R.

APPLICANT: DIIION, Stacey R.

TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS

FILE REFERENCE: 02-02

CURRENT APPLICATION NUMBER: US/10/351,157

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US 60/435,361

PRIOR FILLNG DATE: 2002-12-19

PRIOR FILLNG DATE: 2002-06-14

PRIOR FILLNG DATE: 2002-06-14

PRIOR FILLNG DATE: 2002-01-18

PRIOR FILLNG DATE: 2002-01-18

INUMBER OF SEQ ID NOS: 183

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 38

LENGTH: 2295
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APPLICANT: Gao, Zeren
APPLICANT: Kuijper, Joseph L.
APPLICANT: Dasovich, Maria M.
APPLICANT: Grant, Francis J.
APPLICANT: Presnell, Scott R.
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                                                                                                                                                                                                                                                                                     Grant, Francis J.
Presnell, Scott R.
Whitmore, Theodore E.
Hammond, Angela K.
No. US20030215838Alak, .
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Dasovich, Maria M.
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RESULT 10
US-10-352-554-38
; Sequence 38, Application US/10352554
; Publication No. US20030224487A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
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Best Local Similarity:
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APPLICANT: Kuijper, Joseph L.
APPLICANT: Dasovich, Maria M.
APPLICANT: Grant, Francis J.
APPLICANT: Hammond, Angela K.
APPLICANT: Hammond, Angela K.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
CURENT APPLICATION NUMBER: US/10/352,554
CURRENT APPLICATION NUMBER: US 60/350,325
PRIOR APPLICATION NUMBER: US 60/350,325
PRIOR APPLICATION NUMBER: US 60/375,323
PRIOR APPLICATION NUMBER: US 60/375,323
PRIOR APPLICATION NUMBER: US 60/435,315
PRIOR APPLICATION NUMBER: US 60/435,315
PRIOR APPLICATION NUMBER: US 60/435,315
PRIOR FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 168
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 38
LENGTH: 2295
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LOCATION: (1)...(2295)
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                                TTCCGTGTGAAACCAGTTTTGGGCATCAAACGAATGATTCAAATTGAATGGATAAAGCCT
                                                 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro
                                                                                           ANATCTCATATGACATACTGGAGATTAGAGAACATAGCGAAAACTGAACCACCTAAGATT
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CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/09/892,949
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR PRIOR DATE: 2000-06-29
PRIOR PILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 68
LENGTH: 2295
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Beligned at 150 according
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Query Match:
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; LOCATION: (1)...(2295)
US-10-772-531-68
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US-10-772-531-68
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CURRENT APPLICATION NUMBER: US/10/772,531
CURRENT FILING DATE: 2004-02-05
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APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Kuijper, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
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                                                                                TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn
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US-09-972-708-3
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                                                                    US-10-006-265-4 (1-252)
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Publication No. US20030059871A1
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                    APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: DuBose, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/09/972,708
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
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; SEQ ID NO 3
LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-715-667-3
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US-10-715-667-3
                                                                                                                                                    APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HP)
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/10/715,667
CURRENT APPLICATION NUMBER: US/09/972,708
PRIOR APPLICATION NUMBER: US/09/972,708
PRIOR APPLICATION NUMBER: US/09/972,708
PRIOR TILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
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Matches:
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Sequence 53, Application US/09892949
Publication No. US2003096339A1

GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: Mitmore, Theodore E.
APPLICANT: Mitmore, Toeeph L.
APPLICANT: Maurer, Mark F.
APPLICANT: Maurer, Mark F.
ITITLE OF INVENTION: CYTOXINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
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US-09-892-949-53
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NAME/KEY: CDS
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US-09-892-949-53
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 2903
TYPE: DNA
TYPE: DNA
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APPLICANT: DASOVICH, MATÍA M.
APPLICANT: Grant, Francis J.
APPLICANT: Grant, Francis J.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: No. US20030215638A1ak, Julia E.
APPLICANT: No. US20030215638A1ak, Julia E.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
ITILE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MUL
FILE REFERENCE: 02-02
CURRENT PAPLICATION NUMBER: US/10/351,157
CURRENT PAPLICATION NUMBER: US 60/435,361
PRIOR APPLICATION NUMBER: US 60/435,361
PRIOR FILING DATE: 2002-12-19
PRIOR FILING DATE: 2002-12-19
PRIOR FILING DATE: 2002-16-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 183
SOPTWARE: FastSEQ for Windows Version 4.0
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SEQ ID NO 4
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Publication No. US20030215838A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Gao, Zeren
APPLICANT: Kuijper, Joseph L.
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NAME/KEY: CDS
LOCATION: (497
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TYPE: DNA
ORGANISM: Homo
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Dasovich, Maria M.
Grant, Francis J.
Presnell, Scott R.
Whitmore, Theodore E.
Hammond, Angela K.
No. US20030215838Alak, J
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			1156	220	1096	200	1036	180	976	160

Search completed: February 23, 2005, 20:17:13 Job time: 400.322 secs

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-Q=/G=021/USFTQ spool/US10006265/runat 18022005_094658_22193/app_query.fasta_1.2069
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -ICOPEXT=0
-UNITS=bits -START=1 -END=-1 -MARTRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN-0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006265_@CGN 1 1 7723 @runat 18022005_094658_22193 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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ALIGNMENTS

source 637 bp mRNA linear B0932D09-5 NIA Mouse Unfertilized Egg cDNA Library musculus cDNA clone NIA:B0932D09 IMAGE:30475340 5', CF174021 Email: cdna@lgsun.grc.nia.nih.gov Plate: B0932 row: D column: 09 Seq primer: M13 Reverse Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplif. Mus musculus CF174021.1 EST. Contact: Dawood B. Dudekula Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 11544199 21429098 Genome Res. Mus musculus (house mouse) (bases 1 to 637) quality sequence Location/Qualifiers /organism="Mus musculus" /mol_type="mRNA" 11 (9), 1553-1558 (2001) GI:33283570 stop: Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus EST 25-JUL-2003 (Long 1) Mus , mRNA sequence. amplification Mus.

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US-10-006-265-4 (1-252) x CF174021 (1-637)
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145 ProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAlaPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo (dT) primer [Invitrogen: Sr-pGACTAGTTCTAGTTCTAGTTCTAGTTCTAGT],
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/dev_stage="Unfertilized Egg"
/lab_host="DH10B"
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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Mammalia; Eutheria;
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Plate: B0973 row: F column: 04
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treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LJ-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was
                                                                                                                                                                                                                                                                                                                                                                           Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                          /dev_stage="Unfertilized Egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="NIA:B0973F04 IMAGE:30479295"
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/db_xref="taxon:10090"
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/mol_type="mRNA"
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Best Local Similarity:
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                                                                                                                                                                                                                          AUTHORS
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592 bp mRNA linear EST 19-NOV-2002

K0283D09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus

musculus cDNA clone NIA:K0283D09 IMAGE:30052652 5', mRNA sequence.
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                                           National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, Email: cdna@lgsun.grc.nia.nih.gov Plate: K0283 row: D column: 09
                                                                                                           Contact: Dawood B. Dudekula
Laboratory of Genetics
                                                                                                                                            Other_ESTs: K0283D09-3
                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; N
(bases 1 to 592)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A.,
Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNJ
                             Seq primer: M13 Reverse
                                                                                                                                                             Unpublished (2001)
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                                                                                                                                                                                                                                                                       Eukaryota, Metazoa;
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              quality sequence stop: 592
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Rodentia;
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12
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                                                                             , USA
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MetThrTyrTrpArgLeuGluAsnIle
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                                              CCAGACATCTGCAGTGTTGAAGTACAAGCTCAAAATGGAGATGGTAAAGTTAAATCTGAC
                                                                          ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHis 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: psport1 (Invitrogen); Site_1: Sal1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="NIA:K0283D09 IMAGE:30052652"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
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/strain="C57BL/6J"
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EST 19-NOV-2002 (Long) Mus

Luo, A., Stagg, C.A.,

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ACCESSION
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center University of Washington
401 Queen Anne Avenue North, Seattle, W. Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2180 row: C column: 22
                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                         190
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459 bp DNA linear GSS 16-JUN-1998
HS 2180 A2 B11 MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2180 Col=22 Row=C, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 459)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99380589
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                                                                                       AlaValLysGluSerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGlu 236
                           GluGluGlyLysLeuLeuProAlaIleProValLeuSerThrLeuVal 252
                                                                                                                                                                                                                                                                      ACGATTGTCTCTGTAGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAAAC
                                                                                                                                                                                                                                                                                              ThrValAsnSerThrSerTrpMctGluValAsnPheAlaLysAsnArgLysAspLysAsp 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCACATATTGGCATTTAATCTCCATA 591
    GAAGAANGCAAGCTACTTCCTGCGATTCCCGTCCTGTCTGCTCTGGTG 417
                                                                                                                                                                                 CAAACGTACAACCTCACGGGGCTGCAACCTTNTACAGAATATGTCATAGCTCTGCGATGT
                                                                                                                                                                                                                           GlnThrTyrAsnLeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCys
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CIT Approved Human Genomic Sperm Library D"/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="Plate=2180 Col=22 Row=C"
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345.00
90.79%
89.47%
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Conservative:
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CA560924
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KEYWORDS
                                           Percent Similarity:
Best Local Similarity:
  Query Match:
DB:
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Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C., Martin,P., Alba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_ESTs: K0279C07-3
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus cDNA clone NIA:K0279C07 CA560924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0279 row: C column: 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 479
                                                                                                                                                                                                                                      treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into SalI/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average constructed the standard chemical method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pspORT1 (Invitrogen); Site_1: Sall; Site_2: noti; Mouse cDNA project by the Laboratory of Genetics. National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs.

Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="NIA Mouse Unfertilized Egg cDNA Library (Long)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="NIA:K0279C07 IMAGE:30052254"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6J"
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7.49e-28
342.00
65.62%
51.56%
25.18%
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                                                                                       Length:
Matches:
                                           Conservative: Mismatches:
                       Indels:
479
66
18
34
10
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US-10-006-265-4 (1-252) x CA560924 (1-479)

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RESULT 6
CA555774
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H. Systematic Analyses of NIA Mouse Unfertilized Egg cDNJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA555774 S46 bp mRNA linear K0202F08-5N NIA Mouse Unfertilized Egg cDNA Library musculus CDNA clone NIA:K0202F08 IMAGE:30044899 5', CA555774
                                                                                                                                                                                                                                                                                                                                                                                Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0202 row: F column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                         National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
Other_ESTs: K0202F08-3
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Dawood B. Dudekula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACATCTGCAGTGTTGAAGTACAAGCTCAAAATGGAGATGGTAAAGTTAAATCTGACATC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHisMet 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATAGTGACAATGCTACAGAGGCTTCATATTCTTTTCCCCCGTTCCTGTGCAATGCCCCCA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGTGACTTTGACTTACTCCTATGGAAAA-------AGCAAT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCGACAGAÁTCTGÁCTTGCÁCTTGGAGACCAGAGAÁGGAÁACCAATGATACCAGCTÁT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThrThrAsnSerSer 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGlnTyr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCAAATTCAGCCTGGCAGTCCTGCCGACTAAGCCAGAGAACATTTCCTGCGTCTTTTAC
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                                                                                                                                                                                                                                                                                                                                                              primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 546
/note="Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
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/lab_host="DH10B"
                                                                                                                                                                                                              /mol_type="mRNA"
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                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                    db_xref="niaEST:K0202F08-5N"
db_xref="taxon:10090"
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Rodentia;
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(Long) Mus
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treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)." Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This ideal of the control of th

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JOURNAL
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602850 MARC
CB427282
         1 (bases 1 to 628)
Smith, T.P.L., Roberts, A.J.,
Wray, J.E. and Keele, J.W.
A second set of bovine ESTs
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                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                  AATTATAGTGACAATGCTACAGAGGCTTCATATTCTTTTCCCCGTTCCTGTGCAATGCCC 504
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64.91%
51.75%
22.24%
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                                                                                                                                                                 173 LeuArgPheArgThrValAsnSerThrSerTrpMetGluValAsnPheAlaLysAsnArg 192
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USDA, ARS
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Plate: FQY8019 row: F
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Single pass sequencing. Bases called
trimmed with the aid of the trim_alt
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AlaLeuArgCysAlaValLysGluSerLys---PheTrpSerAspTrpSerGlnGluLys 231
                                                                              LysAspLysAsnGlnThrTyrAsnLeuThrGlyLeuGlnProPheThrGluTyrValIle 212
                                                                                                                                                                                                       TTAAAATTGACATGGACTGATTCACGTTTTAAGAGTTTTATAACA---CTGAAATATGAC 416
                                                                                                                                                                                                                                           IleGlnIleGluTrpIleLysProGluLeuAlaProValSerSerAspLeuLysTyrThr 172
                                                                                                                                                                                                                                                                                  ---AAGCTCAATCCACCÁCATÁTTTTATCAGTCAACAGTTCAAAGGAACTGTCTAGTATT 359
                                                                                                                                                                                                                                                                                                                AlaLysThrGluProProLysIlePheArgValLysProValLeuGlyIleLysArgMet
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                                                         TCATCTACCCGATCTTCATTCACTGTTCAGGACCTTAAACCTTTTACAGAATATGTGTTT
                                                                                                                              ATTCAATATAGGACCAAAGATGCCTCAACTTGGAACCAGGTTCCT---CCTGAAGATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysSerPhePheLeuProArgIleThrIleProAspAsnTyrThrIleGluValGluAla 113
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Box 166, Clay Center, NE 68933-0166, U
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/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: Noi
Library made with RNA pooled From multiple tIssues
including liver, lung, hypothalamus, pituitary, an
placenta/endometrium."
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
Other_ESTs: K0266C03-3
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/strain="C57BL/6J"
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   1.06e-22
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534 AGGATTCGTTGTATGAAGGAAGATGGTAAAGGATATTGGAGTGACTGGAGTGAAGAAGCA 593
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
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Plate: K0266 row: C column: 03
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Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
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treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and Not1 enzymes and cloned into Sal1/Not1 site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pspORT1 (Invitrogen); Site_1: Sall; Site_2: Notl; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs.

Double-stranded cDNAs were synthesized with an Oligo(dT)
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(Long)"
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                          Bource
                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 699)
Adelson,D.L. and Gill,C.A.
Bovine ESTs (Adelson and Gill)
Unpublished (2003)
Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          505
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CB168262.1
EST.
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Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                    Animal Science Dept., TAMU-2471,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGln 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSerCysValTyr 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIle-----
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                                                                                                                                                                                                                                                      9798456970
l: david.adelson@tamu.edu.
                                                                        /mol_type="mxvn
/db xref="taxon:9913"
/tlssue_type="small intestine"
/clone_Tib="CSEQFXN48 small intestine"
/note="Organ: small intestine, Vector: pB
/note="Organ: stre_1: EcoRI, sequence 5'
Site_1: NotI, Site_2: EcoRI, sequence 5'
(5'-NNN....NNN1ssert)
                                              GCGAATTGGAGCTCCACCGCGGTGGCGGCCCCGGGCTCGAG. Sequence 3' of the inserts (AAGAATTCGATATCCAAGCTTATCGATACCGTCGACCTCGAG. normalized RD 2 library, sequenced 3' with M13R primer."
                                                                                                                                                                                         organism="Bos taurus"
|mol_type="mRNA"
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intestine Bos taurus cDNA,
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AUTHORS
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ORGANISM
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VERSION
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Score:
Percent Similarity:
Best Local Similarity:
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DB:
                                                                 TITLE
                                  JOURNAL
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                                                                                                                                                                                                                        musculus
CA561193
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M
1 (bases 1 to 518)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A.,
Martin, P., Aiba, K., Tanaka, T. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA
                Unpublished (2001)
Other_ESTs: K0283F09-3
                                                                                                                                                                                                                                    CA561193
518 bp mRNA linear K0283F09-5N NIA Mouse Unfertilized Egg cDNA Library musculus cDNA clone NIA:K0283F09 IMAGE:30052676 5',
Contact: Dawood B. Dudekula
                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                        CA561193.1
                                                                                                                                                                                                                                                                                                                                                               MetGlyMetThrGluGluGluGlyLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCATCTACCCGATCTTCACTGCTCAGGACCTTAAAACCTTTTACAGA-TATGTGTTT 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTAAAATTGACATGGACTGATTCACGTTTTAAGAGTTTTATAACA----CTGAAATATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaLysThrGluProProLysIlePheArgValLysProValLeuGlyIleLysArgMet 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGAATGCCCTTGGGAAGGTTACCTCAGATCATATCAATTTTGATCCTGTAGATAAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluAsnGlyAspGlyValIleLysSer---HisMetThrTyrTrpArgLeuGluAsnIle 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCACTGTTGATTATCCTCCTGTGTATTTTGTC---AACATTGAAGTCTGGGTAGAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysSerPhePheLeuProArgIleThrIleProAspAsnTyrThrIleGluValGluAla 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheGlyGluLysHisAspAsnCysThrThrAsnSerSerThrSerGluAsnArgAlaSer
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270.50
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Matches:
Conservative:
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67
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                                                                                             Stagg, C.A.
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403

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US-10-006-265-4 (1-252) x CA561193 (1-518)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Genetics
SerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSerCysValTyr 45
                                                                                                                                   TACATTGTGACTTGACTTACTCCTATGGAAAA-----
                                                                                                                                                                                                                  TyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThrThrAsnSer 85
                                                                                                                                                                                                                                                                                                     TACTTCGACAGAATCTGACTTGCACTTGGAGACCAGAGAAGGAAACCAATGATACCAGC 408
                                                                                                                                                                                                                                                                                                                                                                   TyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGln 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTGCAAATTCAGCCTGGCAGTCCTGCCGACTAAGCCAGAGAACATTTCCTGCGTCTTT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCCTCTGGGTGTGAACGCTGGAATAATGTGGACCTTGGCACTGTGGGCATTCTCTTTC 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pSPORT1 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 153-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 148 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: general collaboration of the collaboration of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
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/lab_host="DH10B"
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Scores:
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Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

National Institute on Aging/National Institutes of Health

National Institute on Aging/National Institutes of Health
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Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A., Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 Cassell Drive, Suite 4000, Ba
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0256 row: G column: 09
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                  treated with 74 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
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/db_xref="taxon:10090"
/clone="NIA:K0256G09 IMAGE:30050096"
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/mol_type="mRNA"
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(Long)"
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/lab_host="DH10B"
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/strain="C57BL/6J"
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                 Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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NIH-MGC Project URL: http://mgc.nci.nih.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                           (bases 1 to 1512)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTC 19-NOV-2003
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNI at: http://image.llnl.gov Series: IRAK Plate: 16 Row: k Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6754337 This clone has the following problem: no polyA-tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Gwis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.N., Gibbs, R.A.
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                                                                                                                                      LeuArgPheArgThrValAsnSerThrSerTrpMetGluValAsnPheAlaLysAsnArg 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGATAAACCTACAAATTTGACTTGCATTGTGAATGAGGGGAAGAATATGCTGTGCCAG 672
     ATGTCTCCTCGAACTTCCTTCACTGTGCAGGACCTCAAGCCTTTTACAGAATATGTGTTT 1122
                                 LysAspLysAsnGlnThrTyrAsnLeuThrGlyLeuGlnProPheThrGluTyrValIle 212
                                                                                                                                                                                                                                                 IleGlnIleGluTrpIleLysProGluLeuAlaProValSerSerAspLeuLysTyrThr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- ACAGAGAAGTTTCCTGATTGCCAGTCAAAGCATGGCACT---
                                                                                                     ATCCAATATAGGACCAAAGATGCCTCAACTTGGATCCAGGTCCCTCTT----GAAGATACA
                                                                                                                                                                                                   TTAAAGCTATCATGGGTCAGTTCAGGGCTGGGCGGTCTT---TTAGATCTAAAGTCTGAC 1009
                                                                                                                                                                                                                                                                                                 GTGAAACCCCACCCACCATATAATTTATCAGTGACCAACTCAGAAGAATTATCCAGTATA
                                                                                                                                                                                                                                                                                                                                               AlaLysThrGluProProLysIlePheArgValLysProValLeuGlyIleLysArgMet 152
                                                                                                                                                                                                                                                                                                                                                                                                  GCAGAGAATGCCCTTGGGAAGGTCTCCTCAGAGTCTATCAATTTTGACCCCCGTGGATAAA 888
                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaGluAsnGlyAspGlyValIleLysSerHisMetThrTyrTrpArgLeuGluAsnIle 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTATGGTCAGCTACATGCCCACCTATTATGTC----AACATTGAAGTCTGGGTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysSerPhe---PheLeuProArgIleThrIleProAspAsnTyrThrIleGluValGlu 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheGlyGluLysHisAspAsnCysThrThrAsnSerSerThrSerGluAsnArgAlaSer 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGACCCCGGAAGGGAGACTTACCTTGAAACAAACTACACTTTGAAATCAGAGTGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLysArgThrTyrAla 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Mammary tumor. C3(1)-Tag model.ductal carcinoma. 5 month old virgin mouse." /clone_lb="NCI_CGAP_Mam6" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .1512
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/clone="IMAGE:3598166"
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/strain="FVB/N"
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265.50
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31.25%
19.55%
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Best Local Similarity:
Query Match:
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     229
                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdnaelgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4061 row: G column: 10
Plate: H4061 row: G column: 10
Seg primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other_ESTs: H4061G10-3
Contact: Yong Qian
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ560019 487 bp mRNA linear EST 20-JUN-20
H4061G10-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VanBuren, V., Piao, Y., Dudokula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Alba, K., Hamatani, T., Kargul, G.J., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H. Assembly, verification, and initial annotation of NIA 7.4K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 487)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 12 (12), 1999-2003 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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GCTAGTGGGACCACATACGAAGAC 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 487
                                                                                                                                                                                                                                                                               /lab_host="DH10B"
/Clone lib="NIA Mouse 7.4K cDNA Clone Set"
/clone="Vector: pSPORT1; Site_1: Sall; Site_2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        'dev_stage="mixed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                              clone="H4061G10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       887 bp mRNA linear ES: AGENCOURT 15873120 NIH MGC_219 Homo sapiens cDNA clone IMAGE 30523682 5', mRNA secuence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: NDAM602 row: a column:
High quality sequence stop: 683.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
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1 (bases 1 to 887)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACATTGTGACTTTGACTTACTCCTATGGAAAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACTTCGACAGAATCTGACTTGCACTTGGAGAGCCAGAGGAAACCAATGATACCAGC 408
/tissue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="Ph108 (Tl phage-resistant)"
/clone_lib="NIH_MGC_219"
/clone_lib="NIH_MGC_219"
/cloned_lib="Nector: pYx-Asc; Site_1: EcoRI; Site_2: NotI;
/note="Wector: pYx-Asc; Site_1: EcoRI; Site_2: NotI;
/ibrary is oligo-dT primed and directionally cloned
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according tomRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
0.5-Ikb. Adaptors 5'(AATTAGGGAGGG)3' and 5'd
(CCTCGTGCGG)3' 3' 3' Linker sequence - GCGGCCCTGAGAGGC T18.
Sequencing primers 3'end: T3 promoter primer 5'd
(ATTAACCTCACTAAAGGGA)3'. 15 S'End: T7 promoter primer 5'd
(ATTAACCTCACTAAAGGGA)3'. 5' End: T7 promoter primer 5'd
(TAATAGGACTCACTATAGGGG)3'. Library was constructed in the
laboratory of M. Bento Soares. Average insert size 2-3kb.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:30523682"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Alignment Scores:

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REFERENCE
AUTHORS
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BC071555
LOCUS
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Best Local Similarity:
Query Match:
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                              BC071555
                                                                                                                                                           Eukaryota;
                                                                                                                                                                                           Homo
                                                                                                                                                                                                                           BC071555.1
                                                                                                                                                                                                                                                           errors.
                                                                                                                                                                                                                                                                                                                                                                                   PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAGAC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCAATTTTGATCCTGTATATAAAGTG---AAGCCCAATCCGCCACATAATTTATCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGATGGTAAAGGGAAACACACTTGGAGACAAACTTCACTTTAAAATCTGAATGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGAAAAACCTAAAAATTTGAGTTGCATTGTGAACGAGGGGAAGAAAATGAGGTGTGAG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
                                                                                                                    nmalia, Eutheria, (bases 1 to 5264)
                                                                                                                                                                                         sapiens (human)
                                                                                                                                                                                                                                                                           sapiens cDNA clone
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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51.85%
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Indels:
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US-10-006-265-4 (1-252) x BC071555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortlum/LLNL at: http://image.llnl.gov Series: IRAK Plate: 167 Row: a Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28610146 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I. M.A.G. E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human (Center, Stanford University School of Medicine, Stanford, (Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                      CAGAAAAACCTAAAAATTTGAGTTGCATTGTGAACGAGGGGAAGAAAATGAGGTGTGAG
                                                                                                                                                          ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
TGGGATGGTGGAAGGGAAACACTTGGAGACAAACTTCACTTTAAAATCTGAATGGGCA 640
                                                              TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg
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/tissue_type="Testis"
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/mol_type="mRNA"
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ThrTyrAlaPheGlyGlu-----

-LysHisAsp-----AsnCysThrThrAsn

Search completed: February 23, 2005, 19:23:48 Job time: 2324.44 secs

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
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-DB=GenEmbl -QFMT=fastap -SUPFIX=rge -MINMATCH=0.1 -LOOFCL=0 -LIST=45
-DOCALIGN=5 -START=1 -END=-1 -MARTX*=blosum62 -TRANS=human10.cdi -LIST=45
-DOCALIGN=200 -TRATS_CORE=pct -THR_MAX=100 -THR_NI=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10006265 @CGN 1 11209 @runat 18022005 094657 22181 -NCPU=6 -ICPU=3
-NO MYAD -LARGEQÜERY -NEG_SCORES=0 -MART -DSPBLÖCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XOAPOP=10 -XOAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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PD 14-DEC-2000 WO 2000JP003556
PF 01-JUN-2000 WO 2000JP003556
PR 02-JUN-1999 JP 99P 217797 PI
MASATSUGU MAEDA,NORIKO YAGUCHI
PC C12N15/12,C12N5/10,C07K14/715,C07K16/28,C12P21/02,G01N33/53,
PC G01N33/566
Location/
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1 (Dases 1 to 2119)

Maeda, M. and Yaguchi, N.

Novel hemopoietin receptor protein, NR10

Patent: WO 0075314-A 14 14-DEC-2000;

CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU
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Alignment Scores: 1.34e-305 Length: 2903 Score: 3528.00 Matches: 662 Conservative: 0 Best Local Similarity: 100.00\$ Conservative: 0 Query Match: 60.00\$ Mismatches: 0 Gaps: 0 US-10-006-265-17 (1-662) x AX365201 (1-2903) Qy MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20 DB: 0 Qy MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20 MetLysLeuSerProGlnProSerCysValAsnLeuGagarGaTGTGGACCTGGGCACTG 556 Qy MetLysLeuSerProGlnProSerCysValAsnLeuProAlaLysProGluAsn 40 MetLysLeuSerProGlnProSerCysPalaCysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40 MetLysLeuSerProGlnProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40 MetLysLeuSerProGlySerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40 MetLysLeuSerProGlySerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40 MetLysLeuSerProGlySerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40 MetLysLeuSerProGlySerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40 MetLysLeuSerProGlySerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40 MetLysLeuSerProGlySerLeuCysLysProGluAsn 40 MetLysLeuSerProGlySerLeuCysLysProGluAsn 40 MetLysLeuSerProGlySerLeuCysLysProGluAsn 40 MetLysLeuSerProGlySerLeuCysLysProGlySerLeuCysLysProGlyManachanachanachanachanachanachanachanac	/mol_type="unassigned DNA" /db_xref="taxon:9606" /db_xref="taxon:9606" /octe="unassigned protein product" /codon start=1 /proteIn id="cAp23791.1" /db_xref="GI:18696956" /translation="MKLSPQPSCVNLGMMWTWALHMLPSLCKFSLAALPAKPENISCV YYYRKHLTGTWSPGKETSTYQTYVRRTYAFGSKHNCTTNSSTSEKRASCSFFLPRLT IPDNYTIEVPAENGODLYKSHMYTWARTENIAKTEPPKIFRKFVLGALKRMIQIEMIKP ELAPVSSDLKYTLRFRTVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVIALRCAV KESKFWSDWSQEKMGMTEEDEAPCGLELHLGGESEFVVNLTGLQPFTEYVIALRCAV KESKFWSDWSQEKMGMTEEDEAPCGLELHLGGESFFVSNISGKSFVATLRIPAI GEKSFQCLEVMQACVAEDGLVYKMQSSALDVNTWMIEWFDVDSEFTTLSWESVSQAT NWTIQQDKLKPFMCYNISVFMLHDKVGSPSIQAYAKEGVPSEGPETKURIGVKTV TITMKEIFKSERKGIICNYTIFYQAEGKGESKTVSSILQVGLESLKRKTSYIVQVM ASTSAGGTMGTSINFKTLSFSVFBILLTTSLIGGGLLILITUTANGELKKENKTHLC WPTVPNPAAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDKLVVN FGNVLQEIFTDEARTGQENNLGGEKNGTRILSSCFTSI"	Qy 661 SerIle 662
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Homo sapiens interleukin 31RA splice variant
complete cds, alternatively spliced.
AV499342
   15184896
2 (bases
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Dillon, S.R., Sprecher, C., Hammond, A., Bilsborough, J.,
Rosenfeld-Franklin, M., Presnell, S.R., Haugen, H.S., Maurer, M.,
Harder, B., Johnston, J., Bort, S., Mudri, S., Kuijper, J.L.,
Bukowski, T., Shea, P., Dong, D.L., Dasovich, M., Grant, F.J.,
Lockwood, L., Levin, S.D., LeCiel, C., Waggie, K., Day, H., Topouzis, S.,
Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parrish-Novak, J. and
                                                           dermatitis in mice Nat. Immunol. 5 (7),
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                    Interleukin 31, a cytokine produced by activated T cells, induces
                                                                                                                                                          Gross, J.A.
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Direct Submission
Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc.,
Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc.,
Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc.,
Submission
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                               IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle
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   ATAACGATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATT
                                                                                                                       KESKFWSDWSQEKMGMTEEEAPCGLELMRVLKPAEADGRRPVRLĪMKKARGAPVLEKT
LGYNINY PESINTILTETMNTINQQLELHLGGSESWINGNIS IPAILGKSPVATLRI PAI
QEKSPOCIEVMQACVAEDQLIVYKMGSSALDVIMM EWPPDVDSEPTTLSWESVSQAT
NWTIQQDKLKPFWCYNIS VYPMLHDKVGEPYSIQAYAKEGVPSEGPETKVENIGVKTV
TITMKEI PKSERKGII (NYTII FYQAEGGKGFSKTVNSSILQYCLESLKKKTSYIVQVM
ASTSAGGTNGTSINFKTLSFSVFEILLITISLLGGGLLILI (ITVAYGLKKKPNKLTHLO
ASTSAGGTNGTSINFKTLSFSVFEILLITSLLGGGLLILI (ITVAYGLKKKPNKLTHLO
MPTVPNPAESSIATWHGDDFKDKLNLKESDDSVNTEDRILKFCSTPSDKLVIDKLVVN
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/protein_id="AASB6447.1"
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/translation="MKLSPQPSCVNLGMM"
/translation="MKLS
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/note="class I cytokine receptor;
alternatively spliced"
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497. .2485
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/db_xref="taxon:9606"
/chromosome="5"
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|mol_type="mRNA"
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796 100 736 80

 461 GluArgLy8Gly11eI1eCy8A8nTyrThrI1ePheTyrGlnAlaGluGlyGlyLy8Gly 480 	
 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460 	_
421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440 	
 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420 	L
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361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380 	_
 341 CygIleGluValMetGlnAlaCygValAlaGluAgpGlnLeuValValLygTrpGlnSer 360 	
321 LeuGlyLyBSerProValAlaThrLeuArgIleProAlaIleGlnGluLyBSerPheGln 340 	L
 301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320 	
 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300 	
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 221 SerLyBPheTrpSerAspTrpSerGlnGluLyBMetGlyMetThrGluGluAlaPro 240	
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 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160 	
 121 LyBSerHiBMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140 	

CDS	FEATURES	AUTHORS TITLE JOURNAL	RESULT 4 AX36513 LOCUS DEFINITION ACCESSION VERSION VERVHORDS SOURCE ORGANISM	D Qy	אם אם	B &	p Q	D Q	p Q	Оy	D Q	B &	g Q
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/gene="IL3IRA" /note="class I cytokine receptor; huzcytor17x1; alternatively spliced" /codon_start=1 /product="interleukin 31RA splice variant x1" /product="int	## Source 12529 /organism="Homo Bapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="5" /chromosome="5" /map="sq11" gene 12529 /gene="IJ31RA" CDS /fen="IL111" **Torganism="Fenal" CDS /fen="TL1111" /map="g111" CDS /fenal="IL1111" **Torganism="Homo Bapiens" /map="g11" CDS /fenal="IL1111" **Torganism="Homo Bapiens" /map="g11" CDS /fenal="IL1111" **Torganism="Homo Bapiens" /map="g11" /map="g	Interleukin dermatitis Nat. Immunol 15184896 2 (bases 1 Dillon, S.R., Presnell, S.F. Presnell, S.F. Gross, J.A. Johnston, J., Johnston, J., Johnston, J., Johnston, J., Johnston, J., Johnston, J., Gross, J.A. Gross, J.A. Submitted (I) Eastlake Ave	2049 5	643 AsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSerIle
Db 729 GGGCTGCAGCCTTTTACAGAATATGTCATAGCTCTGCGATGTGCGGTCAAGGAGTCAAAG 788 Qy 223 PheTrpSerAspTrpSerGlnGluLysMetThrGluGluGluGluAlaProCysGly 242	609 GCGCCTGTTTCATCTGATTTAAAATACACACTTCGATTCAGGACAGTCAACAGTACCAGC 6 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 2	Oy 103 IleProAbghanTyTThrIleGluValGluAsmGlyAspGlyValIleLysSer 122 Oy 103 IleProAbghanTyTThrIleGluValGluAsmGlyAspGlyValIleLysSer 122 Oy 104 IleProAbghanTyTThrIleGluValGluAsmGlyAspGlyValIleLysSer 122 Oy	Gaps: -006-265-17 (1-662) x AY499339 (1-2529) 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetT	t Local Sim

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GlnAlaThrAsnTrpThrIleGlnGlnAspLys 400	GLAITGAGGICAIGLAGGCTIGCGTGACGACCAGCTAGTGGTGAA erAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAs 	21 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 3	301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTzpValSerMetIleSerTyrAsnSer 320 	281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300	261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280	241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260	221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240	201 LeuThrGlyLeuGlnProbheThrGluTyrVallleAlaLeuArgCysAlaValLysGlu 220	181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200	161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180	141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160 	121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140 	101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120 	81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100 	61 ThrSerTyrThrGlnTyrThrVallysArgThrTyrAlapheGlyGluLysHisAspAsn 80 	41 IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60 	21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
AUTHORS Cosman, D.J., TITLE Hematopoieti	Homo sapie Homo sapie Eukaryota; Mammalia;	<u>н</u>	Qy 660 rSerIle 662 Db 2503 TTCAATA 2509	Qy 641 GlnGlu-AsnAsnLeuGlyo	Qy 621 LeuValValAsnPheGlyAs	Qy 601 ThrGluAspArgIleLeuLy	Oy 581 TrpHisGlyAspAspPheLA	561 2203	1 GlyGl) 3 GGTGGF	521 IleAsr 2083 ATAAAA	Qy 501 ThrSerTyrIleValGlnV 	Qy 481 PheSerLysThrValAsnS 	Qy 461 GluArgLysGlyIleIleC 	Oy 441 LysValGluAsnIleGlyV	421 1783	401 LeuLy: 1723 TTAAA	1663
Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R. receptors hpr1 and hpr2	ns (human) ns Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butheria; Primates; Catarrhini; Hominidae; Homo.	2238 bp DNA linear PAT 16-JUL-2002 from Patent WO0229060. GI:21900585		GlnGlu-AsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysBroTh 660	LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640 	ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620 	TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600 	LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580	GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560 	PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540 	TyrileValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSer 520	LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500 	GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGly 480 	LygValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460 			

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Qy 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280	The control of the co	661 TCAAAGTTCTGGAGTGACTGGAGCCAAGAAAAATGGGAAATGACTGAGGAAGAAGCTCCA	221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaPro	Qy 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220	QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200	Oy 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180	QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160	QY 121 LYSSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140	QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120	QY 81 CYSThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPheDheLeuProArg 100	QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80	Qy 41 IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60	Qy 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40	Qy 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTxpThrTxpAlaLeu 20	US-10-006-265-17 (1-662) x AX467335 (1-2238)	Indels: Gaps:	3.72e-300 Length: 3465.50 Matches: 99.09% Conservati	GIN /db_xref="taxon:9606"	source 12238 /mol type="Homo sapiens" /mol type="unassigned DNA"	JOURNAL Patent: WO 0229060-A 5 11-APR-2002; Immunex Corporation (US)
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621 LeuvaLVBLABRENEGLYASTVALLEUGINGJULIEPRETITASPGJUAJAATGJINTGJY 640 [1 ACAGAAGAACAGATCTTAAAAACCATGTTCCACCCCCAGTGACAAGTTGGTGATTGACAAG	601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuVallleAspLys 620	581 TEPHISCLYASPASPLASELYSEASPLYSEASPASSCHEAUSELSEASPASSSETVALASE OF THE STATE OF T	BI ADATTGACTCATCTGTGTTGGCCCACCGTTCCCAACCTTGCTGAAAGTATAAGCCACA 1	21 1	1 116ASHF1NEDWALLTHEASHF1NESS VALINGEN SECTION TO THE MEASURE SECTION OF THE MEASURE SECTIO	OI ThrSeTTyrileValGinValMetAlaSerThrSerAlaGlyGlyThrAsmGlyThrSer 	81 PRESETLYSTRIVALASRISETSET LELEGIGINTYTGIYLEGILISETLEGILYSAGGLYS 5	BI GAGAGAAAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGGAAAAGGA 1	21	I GIUPTOTYTSETIIGEITALAIYYALAIYSELUGIYYALFIOSIUTIR 4	O1 Leunysprokhelipcyskykaknilesekydilykklometheuniskaspykseigi O1 TTAAAACCTTTCTGGTGCTATAACATCTCTGTGTATCCAATGTTGCATGACAAAGTTGGC 1	1 INTEREST DE SET LE GRANTET GETTE LE SET LE	2 82 2	21 TGCATTGAGGTCATGCAGGCCTGCGTTGCTGAGAGCAGCTAGTGGTGGTGAAGTGGCAAAAGC 1 61 Caralatagagtcatgcaaaagctagctagctagctagagagaga	41 CysileGluvalMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer	321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340 	301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320	841 ATATGGTACTATCCAGAAAGCAACACTAACCTCACAGAAACAATGAACACTACTAACCAG 900	81 CGGTTGTTATGGAAGAAGGCAAGAGGAGGCCCCAGTCCTAGAGAAAAACACTTGGCTACAAC 8

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Scores:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2393)
Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,
Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J.L.,
Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,
Lockwood,L., Levin,S.D., LeCiel,C., Waggie,K., Day,H., Topouzis,S.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
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Homo sapiens interleukin 31RA splice variant x3 (IL31RA) mRNA,
complete cds, alternatively spliced.
AX499341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Eastlake Avenue East, Seattle, WA 98102, USA
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                                                                       NSSTSENRASCSFFLPRITIPDNYTIEVEAENGDGVIKSHMTYWRLENIAKTEPPKIF
RVKPVLGIKRMLGIEWIKPELAEVGSDLKYTLAETTVNSTSWREVNFAKNKNOKNOTY
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alternatively spliced"
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/chromosome="5"
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4.09e-300 3465.50 39.24% 99.09% 98.23% Length:
Matches:
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Mismatches:
Indels:

Gaps:

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Hematopoietin receptors hpr1 and hpr2
Patent: WO 0229060-A 3 11-APR-2002;
Immunex CorporatioN (US)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMMENT OS Homo sapiens (human) PN WO 02077230-A/3 PD 03-OCT-2002 WO 2002JP002769 PF 22-WAR-2002 WO 2002JP002769	to 2952) aguchi, N. and Hasegawa, M. aguchi, N. and Hasegawa, M. ng varinats 02077230-A 3 03-OCT-2002; 02077230-A 3 03-OCT-2002; 030771CAL CO LTD, MASATSUGU MAEDA, NORIKO N	VERSION BD17807.2.1 GI:30016139 VERSION BD17807.2.1 GI:30016139 KEYWORDS WO 02077230-A/3. SOURCE Homo sapiens (human) ORGANISM Homo sapiens ORGANISM Homo sapiens Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	BD178	CY 641 GlnGluAsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysBro 659 .	Qy 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640	1872 TGGCATGGAGATGATTTCAAGGATAAGCTAAACCTGAAGGAGTCTGATGACTCTGTGAAC	Qy 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580	41 GlyGlyGlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsn 	Qy 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540 	QY 501 ThrSerTyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSer 520	QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500	QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGly 480	Oy 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460	Qy 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440	QY 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420

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Percent Similarity:
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PI WASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC C12N15/12, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, G01N33/15, G01N33/50, G01N33/53
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GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg 462	TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal 442			LeuAspyalAsnThrTrpMeElleGluTrpPheBroAspyalAspserGluProInrThr 182		LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342 	GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322 	TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302	LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282 	LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262	PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly 242	GlyLeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGluSerLys 222 	TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202	AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182 	VallysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162 	HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142 	IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122 	ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102

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AspArgIleLeuLysProCysSerThrProSerAspLysLeuVall1eAspLysLeuVal 622
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                                                          ACTTCTGATTTTCTGGATAAGCTAAACCTGAAGGAGTCTGATGACTCTGTGAACACAGAA
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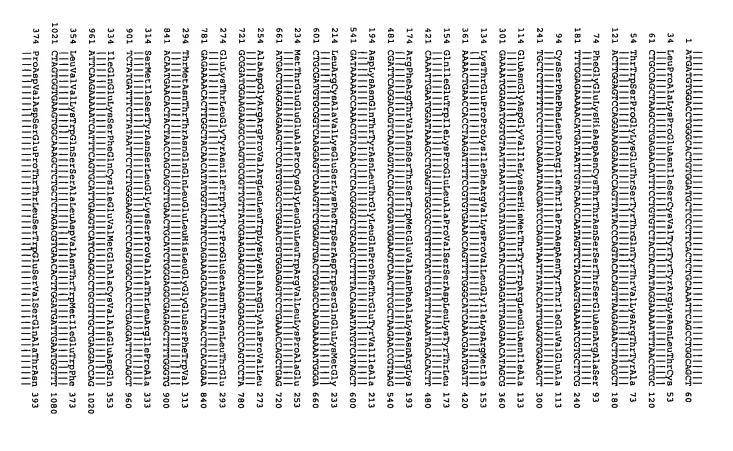
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MetMetTrpThrTrpAlaLeuTrpMetLeuProSerLeuCysLysPheSerLeuAlaAla

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Ghilardi,N., Li,J.,
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Direct Submission
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RFRTYNSTSMMEVNPAKNRKDKNQTYNLTGLQPFTEYVIALRCAYKESKEWSDMSQEK
MGMTEEEAPCGLELMRVLKPAEADGRRPVRLLMKKARGAPVLEKTLGYNIWYYPESNT
NLTETMNTTNQQLELHLGGESFWVSMISYNSLGKSPVATLIPAIQEKSFQCIEVNQA
CVAEDQLVVKMQSSALDVNTMMIEMFPDVDSEPTISMESVSQATNWTIQDDKLKPFW
CYNISVYPMLHDKVGEPYSIQAYAKEGYPSEGPETKVENIGVKTVTITWKEIPKSERK
GIICNYTIFYQAEGGKGFSKTVNSSILQYGLESLKRKTSYIQVWASTSAGGTNGTSI
NFKTLSFSVFSILITITSLIGGGLLILILITAYGLKKFNKLTHLCWPTVPNPAESSIA
TWHODDFXDKLNLKESDDSVMTEDRILKFCSTPSBKLVIIDKLVUMPGNULQBIFTDEA
RTGQENNLGGEKNGYVTCPFRPDCPLGKSFEELPVSPEIPPRKSQYLRSRMPEGTRPE
AKEQLLFSGQSLVPDHLCEEGAPNPYLKNSVTAREFLVSEKLPEHTKGEV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="gp130-like monocyte receptor"
/protein_id="AAM27958.1"
/db_xref="GI:20563277"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="5"
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Conservative:
Mismatches:
Indels:
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1915TATGTGACCTGCCCC 1929	654 IleLeuSerSerCysPro 659	1861 ACAGATGAAGCCAGAACGGGTCAGGAAAACAATTTTAGGAGGGGAAAAGAATGGG 1914	634 ThrAspGluAlaArgThrGlyGlnGluAsnAsnLeuGlyGlyGluLysAsnGlyThrArg 653	1801 GACAAGTTGGTGACAAGTTGGTGGTGAACTTTGGGAAATGTTCTGCAAGAAATTTTC 1860	614 AspLysLeuVallleAspLysLeuValValAsnPheGlyAsnValLeuGlnGluIlePhe 633	1741 GAGTCTGATGACTCTGTGAACACAGAAGACAGGATCTTAAAAACCATGTTCCACCCCCAGT 1800	594 GluSerAspAspSerValAsnThrGluAspArgIleLeuLysProCysSerThrProSer 613	1681 GCTGAAAGTAGTATAGCCACATGGCATGGAGATGATTTCAAGGATAAGCTAAACCTGAAG 1740	574 AlaGluSerSerIleAlaThrTrpHisGlyAspAspPheLysAspLysLeuAsnLeuLys 593	1621 TATGGTCTCAAAAAAACCCAACAAATTGACTCATCTGTGTTGGCCCACCGTTCCCCAACCCT 1680	554 TyrGlyLeuLysLysProAsnLysLeuThrHisLeuCysTrpProThrValProAsnPro 573	1561 ATCCTCATAACTTCTCTGATTGGTGGAGGCCTTCTTATTCTCATTATCCTGACAGTGGCA 1620	534 IleLeuIleThrSerLeuIleGlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAla 553	1501 GGGGGAACCAACGGGACCAGCATAAATTTCAAGACATTGTCATTCAGTGTCTTTGAGATT 1560	514 GlyGlyThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSerValPheGluIle 533		494 LeuGluSerLeuLysArgLysThrSerTyrIleValGlnValMetAlaSerThrSerAla 513	1381 CAAGCTGAAGGTGGAAAAGGATTCTCCAAGACAGTCAATTCCAGCATCTTGCAGTACGGC 1440	474 GlnAlaGluGlyGlyLysGlyPheSerLysThrValAsnSerSerIleLeuGlnTyrGly 493	1321 TGGAAAGAGATTCCCAAGAGTGAGAGAAAGGGGATCATCTGCAACTACACCCATCTTTTAC 1380	454 TrpLysGluileProLysSerGluArgLysGlyIleIleCysAsnTyrThrIlePheTyr 473	1261 CCATCAGAAGGTCCTGAGACCAAGGTGGAGAACATTGGCGTGAAGACGGTCACGATCACA 1320	434 ProSerGluGlyProGluThrLysValGluAsnIleGlyValLysThrValThrIleThr 453	1201 ATGTTGCATGACAAAGTTGGCGAGCCATATTCCATCCAGGCTTATGCCAAAGAAGGAGGCGTT 1260	414 MetLeuHisAspLysValGlyGluProTyrSerIleGlnAlaTyrAlaLysGluGlyVal 433	1141 TGGACGATCCAGCAAGATAAATTAAAACCTTTCTGGTGCTATAACATCTCTGTGTATCCA 1200	394 TrpThrileGlnGlnAspLysLeuLysProPheTrpCysTyrAsnIleSerValTyrPro 413	1081 CCGGATGTGGACTCAGAGCCCACCACCCTTTCCTGGGAATCTGTGTCTCAGGCCACGAAC 1140

Search completed: February 23, 2005, 15:25:27 Job time: 8440.27 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spcol/US10006265/runat 18022005_094657_22172/app_query.fasta_1.2069
-Q=/cgn2 1/USPTO_spcol/US10006265/runat 18022005_094657_22172/app_query.fasta_1.2069
-DB=N_Geneseq_16Dec04 -OpMT=fastap -SUFFIX=rng -MINMATCH=0.1 -ICODECL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006265_@CGN 1 1 1098_ext -HEAPSIZE=500 -MINLEN=0 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                          Result
No.
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Listing first 45 summaries
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Copyright (c) 1993 - 2005 Compugen Ltd.
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4007.918 Million cell updates/sec
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Aac92350 Human hae
Aba93808 Human zcy
Add68146 Human zcy
Ad126569 Human cyt
Aba93803 Human zcy
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ADB73210
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ABA93768
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ABA93804
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ADB87130
Adl26671 Human cyt
Abg83363 Human NR1
Aac92337 Human Nae
Abg83363 Human nee
Aba93767 Human zcy
Adl26673 Human neyt
Add3673 Human nee
Acf36434 Human NR1
Abg83366 Human NR1
Abg83366 Human NR1
Abg83369 Human NR1
Abg83369 Human zcy
Adl26685 Human zcy
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Adl26687 Human zcy
Adl26687 Human pco
Ab186257 Human pro
Ab18627 Human pro
Ab18627 Human pro
Ab18627 Human pro
Adb87310 Novel hum
Adb87328 Novel hum
Adb873310 Novel hum
Adb73328 Novel hum
Adb73310 Novel hum
Adb873310 Novel hum
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ALIGNMENTS

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RESULT 1
AAC92350
 Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10; immunoregulation; haematopoietic cell regulation; transmembrane; immune disorder; haematopoietic disorder; autoimmune disease; allergy;
 Maeda M,
                                              02-JUN-1999;
30-JUL-1999;
                                                                               01-JUN-2000; 2000WO-JP003556
                                                                                                       14-DEC-2000.
                                                                                                                             WO200075314-A1
                                                                                                                                                    Homo sapiens.
                                                                                                                                                                          metal allergy; pollen allergy; ss.
                                                                                                                                                                                                                                    Human haemopoietin receptor protein NR10.3 encoding cDNA SEQ
                                                                                                                                                                                                                                                                                  AAC92350;
                                                                                                                                                                                                                                                                                                        AAC92350 standard; cDNA; 2119
                                                                                                                                                                                                                                                           26-MAR-2001 (first entry)
                        (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Yaguchi N;
                                               99JP-00155797.
99JP-00217797.
                                                                                                                                                                                                                                                                                                        BP.
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Alignment
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The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral. Cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders. Agonists or antizorderoral antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral
                                                                                                                                                  Isolated polynucleotide encoding a useful for treating and diagnosing spleenic, blood or bone disorders.
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                                                                         The invention relates to a novel isolated zcytor17 ligand polypeptide. A polypeptide of the invention has antiinflammatory, dermatological, immunosuppressive, and antimicrobial activity, and may have a use in a vaccine. The polypeptide is useful for treating inflammatory diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicaemia, toxic shock syndrome or infectious diseases. The present sequence is used in
                                                                                                                                                                                                                                                                                                                                         New zcytor17 ligand polypeptides, useful for treating inflammatory diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn disease, atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia.
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19-DEC-2002; 2002US-0435315P
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The invention describes an isolated multimeric or heterodimeric cytokine creceptor (I) having at least one polypeptide having 90 percent sequence condentity with a 732 (S1) or 649 (S2) amino acid sequence given in specification, and where (I) binds a ligand comprising a 164 (S3) amino acid sequence, given in specification, or at least one polypeptide comprising residue 20-227 of (S1). (I) is useful for killing cancer cells and producing an antibody to (I) and a cytokine-binding domain of a class I cytokine receptor. A composition (C1) comprising (I) and a cytokine-binding domain of a class I cytokine receptor and a vehicle is useful for : reducing haematopoietic cells and hematopoietic progenitor cells in a mammal; inhibiting zcytor171ig-induced proliferation or differentiation of hematopoietic cells and hematopoietic progenitor cells; reducing cytor171ig-induced inflammation; treating a mammal afflicted with an inflammatory disease in which zcytor171ig plays a role. The disease is a chronic inflammatory disease such as inflammatory bowel disease. Chronic inflammatory disease is acute inflammatory disease such as endotoxemia, septicaemia, toxic shock syndrome and infectious disease.
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                                                                                 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys
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                                                     The present invention describes a cytokine receptor designated zcytor17. Caytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 cartivines are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections. They are also useful for including certain viral infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the cemplification of the present invention
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29-JUN-2000;
08-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polynucleotide encoding a cytokine receptor zyctor17 which useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 190-194; 235pp; English
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03 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322 	y 263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsmIleTrp 282	9 TTCTGGAGTGACTGGAGCCAAGAAAAAATGGGAATGACTGAGGAAGAAGCTCC. 3 LeuGluLeuTrpArgValLeuLysproAlaGluAlaAspGlyArgArgProVa.	203 GlyLeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGluSerLys 2	y 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182	Y 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142	Y 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102	43 CysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62 [3 LeuSerProGlnProSerCysValAsnL 	core: 3518.00 Matches: 660 ercent Similarity: 100.00% Conservative: 0 est Local Similarity: 100.00% Mismatches: 0 uery Match: 99.72% Indels: 0 B: Gaps: 0 Caps: 0
RESULT 6 ADL26671 standard; cDNA; 2529 BP. ID ADL26671 standard; cDNA; 2529 BP. XX AC ADL26671; XX		603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuVallleAspLysLeuVal	56 58	1689 TTCAAGACATTGTCAGTGTCTTTGAGATTATCCTCATAACTTCTCTGATTGGTGGA 543 GlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu			1329 CCTTTCTGGTGCTATACATCTCTGTGTATCCAATGTTGCATGACAAAGTTGGCGAGCCA 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal	Qy 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 3	Db 1089 AAGTCTCCAGTGGCCACCCTGAGGATTCCAGCTATTCAAGAAAAATCATTTCAGTGCATT 1: Oy 343 GluvalmetGlmAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAla 3(

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20-MAY-2004

(first entry)

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Creceptor (I) having at least one polypeptide having 90 percent sequence (C identity with a 732 (S1) or 649 (S2) amino acid sequence given in Specification, and where (I) binds a ligand comprising a 164 (S3) amino acid sequence given in Specification, or at least one polypeptide (C acid sequence, given in specification, or at least one polypeptide (C comprising residue 20-227 of (S1). (I) is useful for killing cancer cells and producing an antibody to (I) and a cytokine-binding domain of a class (I cytokine receptor. A composition (C1) comprising (I) and a cytokine-binding domain of a class (I cytokine receptor and a vehicle is useful (for: reducing haematopoietic cells and hematopoietic progenitor cells in a mammal; inhibiting zcytor171ig-induced proliferation or differentiation (C a mammal; inhibiting zcytor171ig-induced proliferation or differentiation (C cytor171ig-induced inflammation; treating a mammal afflicted with an (C inflammatory disease in which zcytor171ig plays a role. The disease is a cut chronic inflammatory disease is an inflammatory bowel disease; a copic dermatitis, eczema and (C chronic inflammatory disease is a cute inflammatory disease such as inflammatory disease such as inflammatory disease.

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C chronic inflammatory disease is acute inflammatory disease such as captor disease.

C chronic inflammatory disease is acute inflammatory disease such as inflammatory disease.
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chronic inflammatory disease such as inflammatory bowel disease,
unicerative colitis, acute inflammatory disease such as endotoxemia,
An immune response inhibiting composition is useful for inhibiting immune response in a mammal exposed to an antigen or pathogen. An inflammatory response inhibiting composition is useful for suppress
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DASOVICH M M.
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PRESNELL S R.
HAMMOND A K.
NOVAK J E.
GROSS J A.
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                                                                        Alignment
                                                                                                                              The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence encodes the human NR10.3 protein from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
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                                                                                                Sequence 4315 BP;
                                                                                                                       present invention
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standard; CDNA;

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haemopoietin receptor protein NR10.1 encoding CDNA SEQ H NO:1.

Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10; immunoregulation; haematopoietic cell regulation; transmembrane; immune disorder; haematopoietic disorder; autoimmune disease; al allergy; pollen allergy; 88.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human haemopoietin receptor protein (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haematopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the identification of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies such as metal and capable of the capable of the capable of the capable of the capable of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies such as metal and
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30-JUL-1999;
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                        Isolated polynucleotide encoding a useful for treating and diagnosing spleenic, blood or bone disorders.
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The present invention describes a cytokine receptor designated zcytor17. CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, cantirheumatic, antiarthritic and muscular activities. The zcytor17 CC proteins are useful for treating and diagnosing lymphoid, immune, cytotor17 antibodies are useful in stimulating cell-mediated immunity and czytor17 antibodies are useful in stimulating cell-mediated immunity and cfor stimulating lymphocyte proliferation, such as in the treatment of infections. They are also useful for inducting cytotoxicity and for infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, canceritis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the Sql1 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the cytory.
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Best Local S: Query Match: DB:

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(1-662) x ABA93767

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Gaps: Mismatches: Indels:

Percent Similarity: Best Local Similarity:

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Length: Matches: Conservative:

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Novel multimeric or heterodimeric cytokine receptors useful for treating chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, acute inflammatory disease such as endotoxemia, septicemia.

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14-JUN-2002; 2002US-0389108P
19-DEC-2002; 2002US-0435361P
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(HAMM/)
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WHITMORE T E.
HAMMOND A K.
NOVAK J E.
GROSS J A.
DILLON S R.
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DASOVICH M M.
GRANT F J.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated multimeric or heterodimeric cytokine cc receptor (1) having at least one polypeptide having 90 percent sequence cidentity with a 732 (S1) or 649 (S2) amino acid sequence given in CC specification, and where (1) binds a ligand comprising a 164 (S3) amino acid sequence given in Specification, or at least one polypeptide CC comprising residue 20-227 of (S1). (1) is useful for killing cancer cells CC and producing an antibody to (1) and a cytokine-binding domain of a class I cytokine receptor and a vehicle is useful CC binding domain of a class I cytokine receptor and a cytokine-comprising (1) and
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                                                       TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn
                                                                                                      AAGACAGTCAATTCCAGCATCTTGCAGTACGGCCTGGAGTCCCTGAAAACGAAAGACCTCT
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Percent Similarity: Best Local Similarity:

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Query Match:

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CC metastasis, osteoporosis resulting from an excess of bone-resorbing and CC diseases such as cell proliferation, metabolic and reproductive hormone CC related conditions. They are useful for treating wadical conditions and CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, CS squamous cell carcinoma), haematologic disorders e.g., adenocarcinoma (for example, breast cancer), CC squamous cell carcinoma), haematologic disorders, anaemia (e.g., anaemia cel, ringed sideroblasts or with excess blastic anaemia), myelocypastic syndromes (including refractory anaemia, refractory anaemia cel with ringed sideroblasts or with excess blasts), idopathic thrombocytocypaenic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/ myeloid metaplasia, osteoclast disorders that lead to bone loss such as costeoporosis including post-menopausal osteoporosis, periodontitis regulating in tooth loosening or loss, prosthesis loosening after joint ceplacement, neurodegenerative conditions (e.g., acute polyneuropathy, C myasthenia gravis, chronic fatigue syndrome, transmissible cerabral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful cerebral mammary development and infertility. The present sequence is human HPR1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides HPR1 and HPR2. Sequences of the invention are useful for treating cell proliferation conditions e.g., pancytopaenia, leukopaenia anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporor resulting from a lack of bone-forming cells. They are also useful for treating cell proliferation conditions such as leukaemia and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human and murine hematopoietin receptor useful for treating cell proliferation, hormone related conditions.
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13-OCT-2000; 2000US-0240476P
20-FEB-2001; 2001US-0270282P
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Human type-1 cytokine receptor, GLM-R encoding cDNA

GLM-R; type-1 cytokine receptor; gene therapy; gene mapping; transgenic; gene; ss.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                   26-MAR-2001; 2001JP-00087298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietic receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence encodes the human NR10.4 protein from the
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                                             TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr
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                                                                   The present invention describes haematopoietic receptor NR10 splicing variants (I). (I) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence encodes the human NR10.4 protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                NR10 splicing variants of hematopoietin receptor proteins genes, applicable in searching hematopoietic factors and cremedies for immunological and hematopoietic diseases.
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                                                     present invention
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303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 32 	Qy 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302	Qy 263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsmIleTrp 282	QY 243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262	Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaProCysGly 242	03 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 2 	Qy 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAspCysAspCnThrTyrAsnLeuThr 202	Qy 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182	Qy 143 VallysproValleuGlyIleLysArgMetIleGlnTleGluTrpIleLysProGluLeu 162	QY 123 HismetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142	Qy 103 IleProAspAsnTyrThrIleGluValGluAsnGlyAspGlyValIleLysSer 122	Qy 83 ThragnSerSerThrSerGluagnArgAlaSerCygSerPhePheLeuProArgIleThr 102	Qy 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 82	Qy 43 CysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62	Qy 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42	Qy 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22	-17 (1-662) x ABQ83364 (1-5271)	Alignment Scores: Pred. No.: 8.61e-314 Length: 5271 Score: 9.465.50 Matches: 651 Percent Similarity: 99.24* Conservative: 1 Best Local Similarity: 99.09* Mismatches: 2 Process Mismatches: 2 Process Mismatches: 2 Process Mismatches: 2
RESULT 15 ABQ83366 ID ABQ83366 standard; cDNA; 3072 BP. XX	Db 1990 AACAATTTAGGAGGGGAAAAGAATGGGTATGTGACCTGCCCC 2031	1930 GTGAACTTTGGGAATGTTCTGCAAGAATTTTCACAGATGAAGCCAGAACGC	603 ABPARGILELeulysProcysSerThxProSerAspLysLeuValileAspLysLeuVal	583 GJYASBABPYRELYSASPLYSLEUASILEUJSGIUSERASPASPSETVALASITIRIGIU	563 ThrHisteuCysTrpProThrValProAspEroAlaGluSerSerIleAlaThrTrpHis	543 GlyLeuIeuIleIleIleIleIrThrValAlaTyrGlyLeuLysLysProAshLysLeu	1630 TTCAAGACATTGTCATTCAGTGTCTTTGAGATTATCCTCATAACTTCTCTGATTGGGA	1570	483 LygrinrvalAsinSerSerIleLeuGinTyrcJyLeuGJuSerLeuLysarglysrinrser	463 LygGlyILeIleCygAsnTyrThrILePheTyrGlnAlaGluGlyGlyLysGlyPheSer	130 GAGAACATTGGCGTGAAGACGGTCACGATCACATGGAAAGAGATTCCCAAGAGTGAGAGA	423 TyrSerIleGlnAlaTyrAlaIysGluGlyValProSerGluGlyProGluThrtysVal		383 LeuserTryGluserValserGlnAlaThrAsnTryThrIleGlnGlnAsplysLeuLys	363 LeuAspValAsmThrTrMetIleGluTrpPheProAspValAspSerGluProThrThr	1090 GAGGTCATGCAGGCCTGCGTTGCTGAGGACCAGCTAGTGGTGAAGTGGCAAAGCTCTGCT	323 1030

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                                                                                                                                                                                                                                                                                                                                                                           The present invention describes haematopoietic receptor NR10 splicing variants (1). (1) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietic receptor genes participate in in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence encodes the human NR10.5 protein from the
                                                                                                                                                                                                                                                                                                                                        Sequence 3072 BP;
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                                                                                                                                                                                                                                                                                                                                                                   present invention
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643 AsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysPro 659	623 ValabnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu	603 ASPATGIIELEULYBPTOCYBSETTHTPTOSETASPLYSLEUVAlIIEASPLYSLEUVAl 	588ASPLYSLEUASnLeuLySGluSerASPASPSErValAsnThrGlu	1870 AGGTGCTGGGCCTAGGCCCTAGGGATACAAATGACAAAGTCACTGTCCCTGCCATGAGGCC		563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 	543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu	523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly	503 TyrileValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 	483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 	463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPheSer 	443 GluabnileGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg 	1330 TATTCCATCCAGGCTTATGCCAAAGAAGGCGTTCCATCAGAAGGTCCTGAGACCAAGGTG
	nGlu 642 GGAA 2109	uVal 622 GTG 2049	rGlu 602 AGAA 1989	587 GGCC 1929	587 TGCC 1869	pHis 582 GCAT 1809	BLeu 562 ATTG 1749	YG1Y 542 TGGA 1689	eAsn 522 AAAT 1629	rSer 502 CTCT 1569	eSer 482 CTCC 1509	uArg 462 AGA 1449	GGTG 1389

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Search completed: February 23, 2005, 09:55:29 Job time: 1052.78 secs

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Sequence 1, Appli sequence 25, Appli sequence 3, Appli sequence 3, Appli sequence 1086, Appli sequence 1086, Appli sequence 1086, Appli sequence 1086, Appli sequence 1, Appli sequence 5, Appli sequence 1, Appli sequence 1, Appli sequence 5, Appli sequence 5, Appli sequence 1, Appli sequence 5, Appli sequence 6, Appli

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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17, Appl
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FILE REFERENCE: 06501-070001

CURRENT APPLICATION NUMBER: US/09/700,820C

CURRENT FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: PCT/JP99/02341

PRIOR FILING DATE: 1999-04-90

PRIOR PELICATION NUMBER: JP 10/138652

PRIOR PELING DATE: 1998-05-20

PRIOR FILING DATE: 1998-05-20

PRIOR FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 39

SEQ ID NO 17

LENGTH: 2995

TYPE: DNA
ORGANISM: Mub musculus
           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Patent No. 6610485
GENERRAL INFORMATION:
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Saito, Mikiyoshi
APPLICANT: Ohtomo, Toshihiko
TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
                                                                                                        NAME/KEY: CDS
LOCATION: (29)..(2839)
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US-07-923-976-3

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                                                                     AAAGATAACCTGCTGTGGGTGGAATGGACACCTCCACCTAAACCCGTGAGCAAGTACATC 1444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLysArgThrTyrAla
TTAGAGTGGTGTGTGTCAGAGAACGCACCCTGTGTTGAAGACTGGCAGCAGGAAGAC 150
                                                                                                                                                                                                                                                                                                                AsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeuGluLeuHisLeuGlyGlyGlu
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                                                                                              AlaGluAspGlnLeuValValLysTrpGlnSerSerAlaLeuAspValAsnThrTrpMet
                                                                                                                                           ACCATCCCCAGCCCCACGTCACAGCTGCTTATTCTGTAGTGAATCTTAAAGCATTTCCA 1384
                                                                                                                                                                           ArgIleProAlaIleGlnGluLysSerPheGlnCysIleGluValMetGlnAlaCysVal
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US-09-023-655-1131

; Sequence 1131, Application U:
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   APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
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                                                       THE DETECTION OF BLOOD
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US-09-023-655-1131
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Query Match:
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Best Local Similarity:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH
CLASSIFICATION: DATA:
CLASSIFI
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TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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APPLICATION NUMBER:
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STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                 ACACACAAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT
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                                                                              ATCAATTTTGATCCTGTATATAAAGTG---AAGCCCCAATCCGCCACATAATTTATCAGTG
                                                                                                                               MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
                                                                                                                                                                                   ----AACATTGAAGTCTGGGTAGAAGCAGAGAATGCCCTTGGGAAGGTTACATCAGATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGATGGTGGAAGGGAAACACACTTGGAGACAAACTTCACTTTAAAATCTGAATGGGCA
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                                                                                                         GCTGTGAATGTGGATTCTTCCCACACACAGAATATACATTGTCCTCTTTGACTAGTGACACA
                                                                                                                                                     SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
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                                                                                                   APPLICATION NUMBER: US/08/825,558
FILING DATE: 19-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION: 100
NAME: ESMOND, ROBERT W.
REGISTRATION UNMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.05300(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                         ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VC
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SHARKEY, ANDREW.
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: OP 130 Lacking
NUMBER OF SEQUENCES: 14
                                                                                    SEQUENCE CHARACTERISTICS:
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   TOPOLOGY: 1:
                                TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                           TCACCTCACACTCCTCCAAGGCACAATTTTAATTCAAAAGATCAAATG------TAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGCATTCCTATTGACAACTCTTCTGGGAGTGCTGTTCTGCTTTAATAAGCGAGACCTA 1938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTITTACTACCCCAAAGTTTGCTCAAGGAGAAATTGAAGCCATAGTCGTGCCTGTTTGC 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPhe 481
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                                                                                                                                                                                                                                                                                                                                        ATTAAMAAACACATCTGGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCCAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerTyrileValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
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                                                                                                                                                                                                                                             CysSerThrProSerAspLysLeuVallleAspLysLeuValValAsnPheGlyAsnVal 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGTGAATGTGGATTCTTCCCACACAGAATATACATTGTCCTCTTTGACTAGTGACACA
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                                             GlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSer 661
                                                                                                                                             LeuGlnGluIlePheThrAspGluAla-----ArgThrGlyGlnGluAsnAsnLeuGly 646
                                                                                                                                                                                                -----TTTCCAGAAGATCTGAAATCATTGGAC-----
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     -TCTTCATGCATGTCATCT 2208
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-006-265-17 (1-662) x US-09-312-611-5 (1-2754)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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Patent No. 6380160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,611
FILING DATE: 17-MAY-1999
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0530
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)371-254
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SHARKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gpi30 Lacking
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                             ACACACAAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT 555
                                                                                             SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
                                                                                                                                                                                                                                             TGGGATGGTGGAAAGGGAAACACTTGGAGACAAACTTCACTTTAAAATCTGAATGGGCA 495
                                                                                                                                                                                                                                                                                        TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg 70
                                                                                                                                                                                                                                                                                                                                           CCAGAAAAACCTAAAAATTTGAGTTGCATTGTGAACGAGGGGAAGAAATGAGGTGTGAG 435
                                                                                                                                                                                             ThrTyrAlaPheGlyGlu------LysHisAsp-----AsnCysThrThrAsn 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: STERNE, KESSLER, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : (202)371-2600
(202)371-2540
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                                                                            1579 ACAAAAAAAGTAGGGAAAAACGAAGCTGTCTTAGAGTGGGACCAACTTCCTGTTGATGTT 1638
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462 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPhe 481
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                                                                                                                            ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
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                                                                                                                                                                                                                                 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
                                                                                                                                                                                                                                                                                                                                     LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-08-795-473B-4
; Sequence 4, Application US/08795473B
; Patent No. 6217858
; GENERAL INFORMATION:
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                                                                                               ZIP: 1036

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/795,4731
FILING DATE: 11-FEB-197
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Galun, Eithan
APPLICANT: Nahot, Orit
APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
STREET: 1140 Avenue of the Americas
                     ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
                                                                                                                                                                                                                                                                                                                                                        STREET: 1140 Aven
CITY: New York
STATE: New York
COUNTRY: USA
     REFERENCE/DOCKET NUMBER: 963.1007
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ATTAAAAAACATCTGGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCAGTGG 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TTTCCAGAAGATCTGAAATCATTGGAC-----
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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TELEPHONE: (212)-997-1028
TELEPAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                           1063
                       1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164
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                                                                                                                                      GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
                                                                                                                                                                                          TACTGGAGTGACTGGAGTGAAGAAGCAAGTGGGATCACCTATGAAGATAGACCATCTAAA 1239
                                                                                                                                                                                                                                                                                                                                                         AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAGAC 1119
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                                                                                                                                                                                                                PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys---
                                                                                                                                                                                                                                                                    LeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGluSerLys--- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCAATTTTGATCCTGTATATAAAGTG---AAGCCCAATCCGCCACATAATTTATCAGTG
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                                                          LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
                                                                                                                                                                                                                                                                                                                                                                                                MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
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                     CTCGTGTGGAAGACATTGCCTCCTTTTGAAGCCAATGGAAAAATCTTGGATTATGAAGTG 1359
                                                                                                        GCACCAAGTTTCTGGTATAAAATAGATCCATCCCATACTCAAGGCTACAGAACTGTACAA
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1360 ACTCTCACAAGATGGAAATCACATTTACAAAATTACACAGTTAATGCCACA-----AAA 1413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422
  630 GlnGluIlePheThrAspGluAla-----ArgThrGlyGlnGluAsnAsnLeuGlyGly 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402
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                                           ---TTTCCAGAAGATCTGAAATCATTGGAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTTTACTACCCCAAAGTTTGCTCAAGGAGAAATTGAAGCCATAGTCGTGCCTGTTTGC 213:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGIACATGGTACGAATGGCAGCATACACAGATGAAGGTGGGAAGGATGGTCCAGAATTC 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGAATGGATTTATCAGAAATTATACTATATTTATAGAACCATCATTGGAAATGAAACT 1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGAGAGCAAATGCTATTTGATAACAGTTACTCCAGTATATGCTGATGGACCAGGAAGC 1773
                                                                                  SerThrProSerAspLysLeuValIleAspLysLeuValValAsnPheGlyAsnValLeu
                                                                                                                              AATTTCACTGATGTAAGTGTTGTGGAAATAGAAGCAAATGACAAA-----
                                                                                                                                                                                                              TCACCTCACACTCCTCCAAGGCACAATTTTAATTCAAAAGATCAAATGTATCCAGATGGC
                                                                                                                                                                                                                                                                                            ATTAAAAAAACACATCTGGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCAGTGG 225
                                                                                                                                                                                                                                                                                                                                 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
                                                                                                                                                                                                                                                                                                                                                                               TTAGCATTCCTATTGACAACTCTTCTGGGAGTGCTGTTCTGCTTTAATAAGCGAGACCTA 2193
                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
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                                                                                                                                                                AsnLeuLysGlu---SerAspAspSerValAsnThrGluAspArgIleLeuLysProCys 609
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                                                                                                                                                                                                                                                 ------нівGlyAspAspPheLysAspLysLeu-------
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QY 71 ThrTyralaPheGlyGluLysHisAspAsnCysThrThrAsn 84	Qy 55 TrpSerProGlyLysGluThrSerTyrThrGlnTyrThrValLysArg 70	Qy 35 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54	US-10-006-265-17 (1-662) x US-09-439-856-4 (1-3085)	19.36% Indels: 3 Gaps:	5.08e-65 683.00 46.48%	Š	; LENGTH: 3085 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single	INFORMATION FOR SEQ ID NO. 4:	; REFERENCE/DOCKET NUMBER: 963.1007 ; TELECOMMUNICATION INFORMATION:	ATTORNEY/AGENT INFORMATION: NAME: Davidson, Clifford REGISTRATION NUMBER: 32,	; CLASSIFICATION: ; PRIOR APPLICATION NUMBER: 08/795,473 ; APPLICATION NUMBER: 08/795,473	SOFTWARE: MS-DOS E CURRENT APPLICATION D APPLICATION NUMBER: FILING DATE:	2550	CITY: New York STATE: New York COUNTRY: USA ZIP: 10036	NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Davidson, Davidson STREET: 1140 Avenue of the Am		GENERAL INFOR APPLICANT: APPLICANT:		Db 2446TCTTCATGCATGTCATCT 2463 RESULT 6 RESOLATO-856 A	648 GluLysAsnGlyThrArgIleLeuSerSerCysProThrSer :::	Db 2392CTGTTCAAAAAGGAAAAATTAATACTGAAGGACACAGCAGTGGTATTGGGGGG 2445
Db 1774	P.	ь	Oy 382		Qy 342 Db 1534	Qy 322 Db 1474	Db 1414	ь	Qу 282	Qy 262 Db 1300	Qy 242 Db 1240	Qy 223 Db 1180	Qy 204 Db 1120	Qy 184 Db 1063	Qy 164 Db 1006		Db 889 Qy 144		Qy 105 Db 832	Db 81	Qy 8
PTOTYTSETILGCIDALATYPALALYGGIUGLYVALPTOSETUGLYPTOGUTINTUY8	GCAGAGAGCAAATGCTATTTGATAACAGTTACTCCAGTATATGCTGATGGACCAGGAAGC	ATCACAGACTGGCAACAAGAAGATGGTACCGTGCATCGCACCTATTTAAGAGGGAACTTA	4 AGSGARICIGIANAGANAIAIRIACIIGAGIGGIGIGIIAIACAGAIANAGCACCIGI 1853 2 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401	AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr	2 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361 :::	2 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341 4 GGCAAATCAGATGCAGCTGTTTTAACTATCCCTGCCTGTGACTTTCAAGCTACTCACCCT 1533	TGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT	O ACTCTCACAAGATGGAAATCACCATTTACAAAATTACAATTTATTATTGCCACAAAA 1413		2 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281 :::	2 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261	3 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys 241		4 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203 :::::: :::::::::::::::::::::::::::::	4 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183 	::: : ::::::::::::::::::::::::::::::::		MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal	5 ABPABNTYTTNIIEGluValGluAlaGluAbnGlyAspGlyValIIeLysSerHis 123 ::: 2AACATTGAAGTCTGGGTAGAAGCAGAGAATGCCCTTGGGAAGGTTACATCAGATCAT 888	TATTCTACT	85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104

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RESULT 7
US-07-797-556-1
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07797556
Patent No. 5262522
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gearing, TITLE OF INVENTION: TITLE OF INVENTION:
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
APPLICATION NUMBER: US/07/797,556 FILING DATE: 19911122 CLASSIFICATION: 435
                                                                                                                                                                                         ZIP: 98101
                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                 STREET: 51 Uni
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                                                                                                                                                                                                                                                                     E: Immunex Corporation
51 University Street
                                                                                                                                                                                                            USA
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Receptor for Oncostatin M and Leukemia
Inhibitory Factor
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                                                                                     Version #1
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-797-556-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
TISSUE TYPE: hu
IMMEDIATE SOURCE:
CLONE: B10G/pDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: 81ncl ~
TOPOLOGY
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                                                                                                                                                                                                          124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
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    AGTGTTATAATA----CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG 1050
                                                                                                                                                                                                                                                                                           AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGAAAAAACCTAAAAAATTTGAGTTGCATTGTGAACGAGGGGAAGAAAAATGAGGTGTGAG 678
                                         ProvalSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
                                                                                  ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG 993
                                                                                                                          LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
                                                                                                                                                                                                                                                      ---AACATTGAAGTCTGGGTÄGÄÄĞCÄĞÄĞÄÄTGCCCTTGGGAAGGTTACATCAGATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGATGGTGGAAGGGÀÀACÁCACTTGGAGÁCAAACTTCACTTTAAAATCTGAATGGGCA 738
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                                                                                                                                                                     ATCAATTTTGATCCTGTATATAAAGTG----AAGCCCAATCCGCCACATAATTTATCAGTG
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2062 ACTTTTACTACCCCAAAGTTTGCTCAAGGAGAAATTGAAGCCATAGTCGTGCCTGTTTGC 2121
                                                                                                                                                                                                                                                                                                                                         1942 GCTGTGAATGTGGATTCTTCCCACACAGAATATACATTGTCCTCTTTGACTAGTGACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1642 ATCACAGACTGGCAACAAGAAGATGGTACCGTGCATCGCACCTATTTAAGAGGGAACTTA 1701
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                                                                              522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
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US-08-308-881-1
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                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                               FRAGMENT TYPE: NOTIGINAL SOURCE:
TISSUE TYPE: hIMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
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APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin
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                             FEATURE:
NAME/KEY:
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                                                                                        FEATURE
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CITY: Seattle
STATE: WA
                                                           NAME/KEY:
LOCATION:
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TELEFAX: (206) 233-0644
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                                                                                                                      NAME/KEY:
                                                                                                                                                    CLONE: B10G/pDC303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 ThrTyrAlaPheGlyGlu------LysHisAsp------AsnCysThrThrAsn
                                                                                                                                                                                                                                                             LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
                                                                                                                                                                                                                                                                                                      GCACCAAGTTTCTGGTATAAAATAGATCCATCCCCATACTCAAGGCTACAGAACTGTACAA 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
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                                   GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
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                                                                                                                 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
                                                                                                                                                        ACTCTCACAAGATGGAAATCACATTTACAAAATTACACAGTTAATGCCACA-----AAA 140
                                                                                                                                                                                                                                                                                                                                       GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
                                                                                                                                                                                                                                                                                                                                                                                  TACTÉGACTGACTGGAGTGAAGAAGCAAGTGGGATCACCTATGAAGATAGACCATCTAAA 1227
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     GGCAAATCAGATGCAGCTGTTTTAACTATCCCCTGCCTGTGACTTTCAAGCTACTCACCCT 152
                                                                                                                                                                                         TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
                                                                                                                                                                                                                                  CTCGTGTGGAAGACATTGCCTCCTTTTGAAGCCAATGGAAAAATCTTGGATTATGAAGTG
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                                                                               CTGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT
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Patent No. 5891997
GENERAL INFORMATION:
                                                                                                           APPLICANT: Mosley, Bruce
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                     2242 TCACCTCACACTCCTCCAAGGCACAATTTTAATTCAAAAGATCAAATG
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ATTAAAAAACACATCTGGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCAGTGG
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Best Local Similarity:
Query Match:
DB:
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US-09-058-263-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
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NAME/KEY:
LOCATION:
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NAME/KEY:
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ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
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NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft Word, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,263
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APPLICATION NUMBER:
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CLONE: B10G/pDC303
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TEV: 756822
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
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                                               105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His
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482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
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                                                                                                     ACAAAAAAGTAGGGAAAAACGAAGCTGTCTTAGAGTGGGACCAACTTCCTGTTGATGTT 1881
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                                                                 ArgLyaGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPhe 481
                                                                                                                                          ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
                                                                                                                                                                                                                                                                              LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT 1461
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                                                                                                                                                                            CCTGAATCCATAAAGGCATACCTTAAACAAGCTCCACCTTCCAAAGGACCTACTGTTCGG
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RESULT 10
US-09-059-099-1
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                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
                                                                                                                                                                                    TELEX: 756822
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: C
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE:
TISSUE TYPE: h
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APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOTTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: PRIOR APPLICATION DATA:
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                                                                                                                                                   LENGTH: 2369 base pairs
TYPE: nucleic acid
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                                                                                                                 TOPOLOGY:
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51 University Street
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FEATURE:
NAME/KEY:
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CLONE: B10G/pDC303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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                                                         GCACCAAGTTTCTGGTATAAAATAGATCCATCCCATACTCAAGGCTACAGAACTGTACAA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
                                                                                                                                  TACTGGAGTGACTGGAGTGAAGAAGCAAGTGGGATCACCTATGAAGATAGACCATCTAAA 1227
                                                                                                                                                                  PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
                                                                                                                                                                                                                                                                                AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
                                                                                          GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCAATTTTGATCCTGTATATAAAGTG----AAGCCCAATCCGCCACATAATTTATCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACACACAAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT 798
                                                                                                                                                                                                         TGGGATGGTGGAAGGGAAACACACTTGGAGACAAACTTCACTTTAAAAATCTGAATGGGCA 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg
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Matches:
Conservative:
Mismatches:
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1402 CTGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT 1461
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                                                                                                                                                                                                                                                                                                                                                                             2122 TTAGCATTCCTATTGACAACTCTTCTGGGAGTGCTGTTCTGCTTTAATAAGCGAGACCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1822 ACAAAAAAGTAGGGAAAAACGAAGCTGTCTTAGAGTGGGACCAACTTCCTGTTGATGTT 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1762 CCTGAATCCATAAAGGCATACCTTAAACAAGCTCCACCTTCCAAAGGACCTACTGTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1702 GCAGAGAGCAAATGCTATTTGATAACAGTTACTCCAGTATATGCTGATGGACCAGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1642 ATCACAGACTGGCAACAAGAAGATGGTACCGTGCATCGCACCTATTTAAGAGGGAACTTA 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               502 SerTyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402 LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                         542 GlyGlyLeuLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGTACATGGTACGAATGGCAGCATACACAGATGAAGGTGGGAAGGATGGTCCAGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGTGAATGTGGATTCTTCCCACACAGAATATACATTGTCCTCTTTGACTAGTGACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTITIACTACCCCAAAGTTTGCTCAAGGAGAAATTGAAGCCATAGTCGTGCCTGTTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
                                                                                                                                                                                                                                                                                   ATTAAAAAACACATCTGGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCAGTGG
                                                                                                                                                                                                                                                                                                                                 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
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                                                                                                                                                                                      US-10-006-265-17 (1-662) x US-09-058-264-1 (1-2369)
                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-058-264-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 2614.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
LOCATION:
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NAME/KEY:
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NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26 MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Imm
STREET: 51 Uni
CITY: Seattle
STATE: WA
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FILING DATE: 12-SEP-
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/058,264
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                                                                                            619 CCAGAAAAACCTAAAAATTTGAGTTGCATTGTGAACGAGGGGAAGAAAATGAGGTGTGAG
679 TGGGATGGTGGAAGGGAAACACACTTGGAGACAACTTCACTTTAAAATCTGAATGGGCA
                          55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg
                                                                                                                                   35 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
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51 University Street
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244..309
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678.50
48.44*
29.34*
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-058-264-1 RESULT 11

Sequence 1, Application US/09058264
Patent No. 6010886
GENERAL INFORMATION:

APPLICANT:

Mosley, Cosman,

David J. Bruce

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1051 AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAGAC 110
                          1702 GCAGAGAGCAAATGCTATTTGATAACAGTTACTCCAGTATATGCTGATGGACCAGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal
                                                                                                                                                                                                                                                                                                                         GTAATGGATCTTAAAGCATTCCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 158
                                                                                                                                                                                                                         LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACTGGAGTGACTGGAGTGAAGAAGCAAGTGGGATCACCTATGAAGATAGACCATCTAAA 1227
                                                                                                                                                                                                                                                                AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
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                                                                      LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu
                                                                                                                                                                       ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu
                                                                                                                                                                                                                                                                                                                                                                        IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
                                                                                                                                                                                                                                                                                                                                                                                                                             GGCAAATCAGATGCAGCTGTTTTAACTATCCCTGCCTGTGACTTTCAAGCTACTCACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGACAGTAAATCTCACAAATGATCGCTATCTAGCAACCCTAACAGTAAGAAATCTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTCTCACAAGATGGAAATCACATTTACAAAATTACACAGTTAATGCCACA-----AAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGTGTGGAAGACATTGCCTCCTTTTGAAGCCAATGGAAAAATCTTGGATTATGAAGTG
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APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Recepto)
NUMBER OF SEQUENCES: 11
                  APPLICATION NUMBER: US 08/249
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft WO CURRENT APPLICATION DATA:
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CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOPTWARE: Microsoft Word, Version
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/455,962 FILING DATE: CLASSIFICATION:
TELEPHONE:
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51 University Street
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  (206) 233-0644
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Percent Similarity:
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Pred. No.:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
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NAME/KEY:
LOCATION:
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TISSUE TYPE: human
IMMEDIATE SOURCE:
CLONE: B10G/pDC303
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LOCATION:
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619 CCAGAAAAACCTAAAAATTTGAGTTGCATTGTGAACGAGGGGAAGAAAATGAGGTGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                  AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His
                                         AGCCAGATTCCT----CCTGAAGACACAGCATCCACCCGATCTTCACTGTCCAAGAC 1107
                                                                                                                     AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
                                                                                                                                         ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp
                                                                                                                                                                                             ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG
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LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys---
                                                                           MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
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19.23%
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Matches:
Conservative:
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                                                           2122 TTAGCATTCCTATTGACAACTCTTCTGGGAGTGCTGTTCTGCTTTAATAAGCGAGACCTA 2181
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562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
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                                                                                               GlyGlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
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NAME/KEY: mat_peptide COCATION: 3102369	NO N-termin S: human p: E: pDC303	REGISTRATION NUMBER: 32,172 REFERENCE/DOCKET NUMBER: 2614-WO TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430 TELEFAX: (206) 587-0430 TELEFAX: (206) 233-0644 TELEX: 756822 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2369 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA to mrna	KRARSE REI	: 11 ESS: ex Corporation rsity Street ORM: ppy disk pc-DOS/MS-DOS	Qy 582
Oy 302 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsmSerLeu 321	1228 GCACCAAGTTTCTGGTATAAATAGATCCATCCCATACTCAAGGCTACAGAACTGTACAA 262 LeuLeuTxpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle	Qy 184 MetGluValAsnPheAlaLysAsnLysAsnClnThrTyrAsnLeuThrGly 203 Db 1051 AGCCAGATTCCTCCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAGAC 1107 Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222 :::	Qy 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143 ::::::::::::::::::::::::::::::::::::	Qy 71 ThrTyrAlaPheGlyGluLy8HisAspAsnCy8ThrThrAsn 84 ::: :::	Query Match: 19.23% Indels: 39 DB: 5 Gaps: 14 US-10-006-265-17 (1-662) x PCT-US95-06530-1 (1-2369) Qy 35 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54 [

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US-08-825-558-3
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/0882558
Patent NO. 5965724
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
                                                                                                                                                                                                                                                                         APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp 130 Lacking
NUMBER OF SEQUENCES: 14
                                                                                                                                                 COUNTRY: UZIP: 20005
                                                                                                                                                                                                    CITY: WASHINGTON
   FILING DATE:
                      APPLICATION NUMBER:
                                                                                                                                                                                                                       STREET:
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Best Local Similarity:
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TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
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ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1977 base pairs
TYPE: nucleic acid
CTBANTERISTICS:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His
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AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAGAC 864
                                                                                                                                                                                                                       AGTGTTATAATA---CTAAAATATAACATTCAATATAGGACCAAAGATGCCTCAACTTGG
                                                                                                                                                                                                                                                                                            ATCAACTCAGAGGAACTGTCTAGTATCTTAAAATTGACATGGACCAACCCAAGTATTAAG
                                                                                                                                                                                                                                                                                                                                  LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla
                                                                                                                                                                                                                                                                                                                                                                       ATCAATTTTGATCCTGTATAAAAGTG---AAGCCCAATCCGCCACATAATTTATCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AACATTGAAGTCTGGGTAGAAGCAGAGAATGCCCTTGGGAAGGTTACATCAGATCAT
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                                                                          LeuGlnProPheThrGluTyrVall1eAlaLeuArgCysAlaValLysGluSerLys---
                                                                                                                                                                                 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly
                                                                                                                                                                                                                                                  ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerTyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAATGGATTTATCAGAÄÄTTÄTÄCTÄTÄTTTÄTÄGAACCATCATTGGÄAATGAAACT 1698
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Best Local Similarity:
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US-09-312-611-3
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PATENT NO. 6380160
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
APPLICANT: DELLOW, KIMBERLEY A.
ATITLE OF INVENTION: GP130 Lacking the Transmembrane Domain NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,611
FILING DATE: 17-MAY-199
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
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105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
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                                                                                                                                                                                ACACACAGTTTGCTGATTGCAAAGCAAAACGTGACACCCCCACCTCATGCACTGTTGAT 555
                                                                                                                                                                                                                                ThrTyrAlaPheGlyGlu------LysHisAsp------AsnCysThrThrAsn 84
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Matches:
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Indels:
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1843 TTAAAAAACAC
562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
1840
542 GlyGlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
1819 ACTITTACTACCCCAAAGTTT
522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
1759 TTGTACATGGTACGAATGGCAGCATACACAGATGAAGGTGGGAAGGATGGTCCAGAATTC 1818
502 SerTyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
1699 GCTGTGAATGTGGATTCTTCCCACACAGAATATACATTGTCCTCTTTGACTAGTGACACA 1758
482 SerLysThrValAgnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501

Search completed: February 23, 2005, 19:36:50 Job time: 349.791 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q-[cgn2 1/USPTO_spool/US10006265/runat_18022005_094659_22236/app_query.fasta_1.2069
-Q=[cgn2 1/USPTO_spool/US10006265/runat_18022005_094659_22236/app_query.fasta_1.2069
-DB=PublIshed_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPECI-0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST-45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US10006265 @CGN 1 1 1175 @TUNAT 18022005 094659_22236
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORE=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOD=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length:
Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/USO0E_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO0E_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO0E_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 US-10-006-2 Sequence Publicati GENERAL I. APPLICAN APPLICAN TITLE OF FILE REF CURRENT CURRENT PRIOR AP PRIOR AP PRIOR AP PRIOR FI PRIOR AP PRIOR FI		11111111111111111111111111111111111111	Result No.
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lleThrileProAspAsnTyrThrileGluValGluAlaGluAsnGlyAspGlyValile 12 	81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 10	ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 	41 IleSerCyBValTyrTyrTyrArgLyBAsnLeuThrCyBThrTrpSerProGlyLyBGlu 	21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40 	1 MetLysLeuSerProGlnProSerCysValAsn 1	/ Match: 100.00% Indels: 10 Gaps:	Pred. No.: 0 Length: 2903 Score: 3528.00 Matches: 662 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismarches: 0	LOCATION: S-09-892-949-	TYPE: DNA ; ORGANISM: Homo sapiens ; PEATURE: ; NAME KEY. CDS	NUMBER OF SEQ ID NOS: 93 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SO ID NO 53 ; LENGTH: 2003	PRIOR APPLICATION NUMBER: US 60/214,955 PRIOR FILING DATE: 2000-06-29 PRIOR APPLICATION NUMBER: US 60/267,963 PRIOR FILING DATE: 2001-08-02	CURRENT APPLICATION NUMBER: US/09/892,949 ; CURRENT FILING DATE: 2001-06-26 ; PRIOR APPLICATION NUMBER: US/09/892 ; PRIOR APPLICATION NUMBER: US/09/214,282 ; PRIOR APPLICATION NUMBER: US/09/214,282	; APPLICANT: Wiljer, Joseph L. ; APPLICANT: Maurer, Mark F. ; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 ; TITLE OF INVENTION: OA-42 TOKINE RECEPTOR ZCYTOR17	APPLICANT: Sprecher, Cindy A. APPLICANT: Presnell, Scott R. APPLICANT: Gao, Zeren APPLICANT: Gao, Zeren	US-09-892-949-53 ; Sequence 53, Application US/09892949 ; Publication No. US20030096339A1 ; GRNERAL INFORMATION:	1991 TCAATA 1	Db 1931 CAGGAAAACAATTTAGGAGGGAAAAGAATGGGACTAGAATTCTGTCTTCCTGCCCAACT 1990	641 GlnGluAsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysProThr
D Qy	dg VQ	gg Qg	Qy dg	da V	מם עס	B &	B &	B &	B &	g Qy	g Qy	B &	B &	D Q	D Qy	B &	da	8
461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGly 480 		421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440 	401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420 	381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThr1leGlnGlnAspLys 400 	361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380 	341 CyBIleGluValMetGlnAlaCyBValAlaGluABpGlnLeuValValLyBTrpGlnSer 360 	321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGinGluLysSerPheGln 340 	301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320 	281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300 	261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280 	241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260 	221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240 	201 LeuThrGlyLeuGlnDroPheThrGluTyrVallleAlaLeuArgCysAlaValLysGlu 220 	181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnClnThrTyrAsn 200 	161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180 	141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160	857 AAATCTCATATGACATACTGGAGATTAGAGAACATAGCGAAAACTGAACCACCTAAGATT 916	121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluBroProLysIle 140

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US-10-351-157-4

Sequence 4, Application US/10351157

Publication No. US20030215838A1

GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Gao, Zeren
APPLICANT: Lasovich, Maria M.
APPLICANT: Dasovich, Maria M.
APPLICANT: Dasovich, Maria M.
APPLICANT: Dasovich, Maria M.
APPLICANT: Hammond, Angela K.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Hammond, Angela K.
APPLICANT: Oross, Jane A.
APPLICANT: Oross, Jane A.
APPLICANT: Dillon, Stacey R.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MUL.
FILE REFERENCE: 02-02

CURRENT APPLICATION NUMBER: US/10/351,157

CURRENT APPLICATION NUMBER: US/0/35,361

PRIOR APPLICATION NUMBER: US 60/435,361

PRIOR FILING DATE: 2002-12-19

PRIOR APPLICATION NUMBER: US 60/389,108

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 183

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 2903

TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
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  IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
                                                 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu
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                                                                                                            CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal
                                                                                                                                                                                        CTCACGGGGCTGCAGCCTTTTACAGAATATGTCATAGCTCTGCGATGTGCGGTCAAGGAG
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APPLICANT: Sprecher, Cindy A.
APPLICANT: Kuijper, Joseph L.
APPLICANT: Kuijper, Joseph L.
APPLICANT: Cant. Francis J.
APPLICANT: Grant, Francis J.
APPLICANT: Hammond, Angela K.
APPLICANT: Novak, Julia E.
APPLICANT: Novak, Julia E.
APPLICANT: Gross, Jane A.
APPLICANT: Dillon, Stacey R.
TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIG
FILE REFERENCE: 02-01
CURRENT APPLICATION NUMBER: US 60/350,325
PRIOR FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US 60/375,323
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/435,315
PRIOR FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 168
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 2903
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (497)...(2482)
US-10-352-554-4
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Publication No. US20030224487A1
GENERAL INFORMATION:
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                                                                                                                               APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Joseph L.
APPLICANT: Maurer, Mark F.
APPLICANT: Maurer, Mark F.
ITITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILLE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/10/772,531
CCURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/09/892,949
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOPTWARE: FastSEQ for Windows Version 3.0
ENGTH: 2903
TYGE: DNA
                US-10-772-531-53
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 Alignment Scores:
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Publication No. US20040142422A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sprecher, Cindy A. APPLICANT: Presnell, Scott R. APPLICANT: Gao, Zeren APPLICANT: Whitmore, Theodore APPLICANT: Kuijper, Joseph L.
                                                  ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (497)...(248
                                                                                                                      TYPE: DNA
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2357 TTGGTGGTGAACTTTGGGAATGTTCTGCAAGAATTTTTCACAGATGAAGCCAGAACGGGT 2416 641 GlmGluAsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysProThr 660	261 ATGLEULEUTTPLYGLYGRA BATGGLYALAPTOVALLEUGLULYGYTTLEUGLYYYYFAST 2
2297 ACAGAAGACAGGATCTTAAAACCATGTTCCACCCCCAGTGACAAGTTGGTGATTGACAAG 2356 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlepheThrAspGluAlaArgThrGly 640	241 CYBGJYLEBUSHULBUSTYPARYWAILEBUJYBFYCALAGIHAIAABGGIYAFGARGFYCWAI 26
TGGCATGGAGATGATTTCAAGGATAAGCTAAACCTGAAGGAGTC ThrGluAspArgIleLeuLysProCysSerThrProSerAspLy	221 SerLysPheTrpSerAsgTrpSerGInGluLysMetGlyMetThrGluGluGluAlabro 240
	201 LeuThrGlyLeuGlnProPheThrGluTyrVallIeAlaLeuArgCy8AlaValLy8Glu 220
	Qy 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAsnDlysAsnGlnThrTyrAsn 200 27
	Oy 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
n ∩ —i	Oy 141 PheArgValLyBProValLeuGlyIleLyBArgMetIleGlnIleGluTrpIleLyBPro 160
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	Qy 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
	Qy 81 CysThrThrasnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100 bb 737 TGTACAACCAATAGTTCTACAAGTGAAAATCGTGCTTCGTGCTTTTTTCCTTCC
	Qy 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
	Qy 41 IleSerCysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
	Qy 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
16	Qy 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
THE TOTAL TO	Gaps: 0 -265-17 (1-662) x US-10-772-531-53 (1-2903)
321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340 	Pred. No.: 0 Length: 2903 Qy Score: 3528.00 Matches: 662 Db Percent Similarity: 100.00% Conservative: 0 Db Best Local Similarity: 100.00% Mismatches: 0 Db Query Match: 100.00% Indels: 0 Qy

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; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(2108)
US-09-892-949-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45, Application US/09892949
Publication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Toseph L.
APPLICANT: Whitmore, Joseph L.
APPLICANT: MAUTER, MARK F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR APPLICATION NUMBER: US 60/214,963
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
INUMER OF SEQ ID NOS: 93
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 45
LENGTH: 2529
TYPE: DNA
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Best Local Similarity:
Query Match:
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                           ValLysProValLeuGlyIleLysArgMetIleGlnIleGlnTrpIleLysProGluLeu
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                                        TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsmGlyThrSerIleAsm 522
                                                                                             LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer
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Pred. No.: Score: Score: Score: Percent Similarity: 100.00% Best Local Similarity: 100.00% Query Match: 0 99.72% DB: US-10-006-265-17 (1-662) x US-10-351-157-108 (1-2529)	157-	TYPE: DN ORGANISN FEATURE: NAME/KE)	; NUMBER OF SEQ ID NOS: 183 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 108 ; LENGTH: 2529	; PRIOR APPLICATION NUMBER: US 60/389,108 ; PRIOR FILING DATE: 2002-06-14 ; PRIOR APPLICATION NUMBER: US 60/350,325 ; PRIOR FILING DATE: 2002-01-18	CURRENT APPLICATION NUMBER: US/10/351,157 ; CURRENT FILING DATE: 2003-01-21 ; PRIOR APPLICATION NUMBER: US 60/435,361 ; PRIOR FILING DATE: 2002-12-19	EPTOR ZCY		APPLICANT: Gao, Zeren APPLICANT: Kuijper, Joseph L. APPLICANT: Dasovich, Maria M. APPLICANT: Crapt Francis I	Sequence 108, Application US/10351157 ; Bequence 108, Application US/10351157 ; Publication No. US20030215838A1 ; GENERAL INFORMATION: · APPLICATION:	ט נ	643 AsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSerIle	Qy 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642	Db 1929 GACAGGATCTTAAAACCATGTTCCACCCCCAGTGACAAGTTGGTGATTGACAAGTTGGTG 1988	25 5	583 GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu 6	Qy 563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582	Db 1749 GGCCTTCTTATTCTCATTATCCTGACAGTGGCATATGGTCTCAAAAAACCCAACAAATTG 1808	1689 TTCAAGACATTGTCATTCAGTGTCTTTGAGATTATCCTCATAACTTCTCTGATTGGTGGA 1
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RESULT 8
US-10-772-531-45
; Sequence 45, Application US/10772531
; Publication No. US20040142422A1
; Publication No. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZC.
; FILE REFERENCE: 00-42
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PRIOR FILING DATE: 2001-06-26
PRIOR PPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR PILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FBASESEQ for Windows Version 3.0
SEQ ID NO 45
LENGTH: 2529
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CURRENT FILING DATE: 2004-02-05
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NAME/KEY: CDS
LOCATION: (162
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ORGANISM: Homo
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                                                          TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr
                                                                                                                   AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer
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                                             TGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAAACCAAACGTACAACCTCACG
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Matches:
Conservative:
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APPLICANT: Wasda, Masateugu
APPLICANT: Yaguchi, No. US20030125520A11ko
ITITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PRO
FILE REFERENCE: 06501-096001
CURRENT APPLICATION NUMBER: US/10/006,265
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/JP00/03556
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR FILING DATE: 1999-06-02
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEO ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2969
                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-006-265-1
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TYPE: DNA
ORGANISM: Homo
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NAME/KEY: CDS
LOCATION: (523)...
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Score: Percent Similarity: Best Local Similarity	441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleDroLysSer 460 	음 성
US-09-972-708-5 Alignment Scores:	421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440 	용 성
; SEQ ID NO 5 ; LENGTH; 2238 ; TYPE: DNA ; ORGANISM: Homo saj		유 상
CURRENT APPLICATION CURRENT FILING DATI NUMBER OF SEQ ID	381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrlleGlnGlnAspLys 400 	B 상
APPLICANT: Dubose APPLICANT: Wiley, APPLICANT: Wiley, ITITLE OF INTERNATION	361 SerAlaLeuAspValAsmThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380 	용 성
APPLICANT: Immunex APPLICANT: Cosman APPLICANT: Mosley APPLICANT: Mosley	341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360 	유 성
US-09-972-708-5 ; Sequence 5, Application No. US2:	321 LeuGlYLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340 	당 왕
CY 2503 TTCAATA	301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320 	용 성
2443	281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300 	₽ 8
2383	261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280 	9 6
2323	241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260 	B 8
2263	221 SerLyBPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaPro 240 	유 상
5 22 03 5 81	201 LeuThrGlyLeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaValLysGlu 220 	B 8
2143	181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAsnGlysAsnGlnThrTyrAsn 200 	유 성
2083	161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180 	9 6
2023	141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160 	95 VQ
1963	121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140 	A 6
461 1903 481		P & (
_	763 IGTACAACCAATAGTTCTACAAGTGAAAATCGTGCTTCGTGCTCTTTTTTTCCTTCC	8

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Best
Local Similarity:
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sman, David J.
sley, Bruce A.
rd, Timothy A.
Bose, Robert F.
ley, Steven R.
TION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
BATION NUMBER: US/09/972,708
DATE: 2001-10-05
ID NOS: 29
                                                                                  n version 3.1
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Query Match: DB:

US-10-006-265-17 (1-662) x

1002-265-17 (1-662) x US-09-972-708-5 (1-2238) 1 MeLlyaluses-progling-post-cyteral-anneoglymetwer-trythrytalieu 20 Hellyaluses-progling-post-cyteral-anneoglymetwer-trythrytalieu 20 Hellyaluse-post-cyteral-anneoglymetwer-trythrytalieu 20 Hellyaluse-post-cyteral-anneoglymety-post-cytera	
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241 Cyali-denical Trayariyali-deniya Provideni Malaangiliyarga Naprovideni Colori Malaangiliyarga Naprovideni	Percent Similarity: 99.09% Conservative: 2 Dest Local Similarity: 98.73% Mismatches: 3 Dest Watch: 33 Dest Hold Similarity: 98.73% Mismatches: 3 Dest Hold Similarity: 18.73% Mismatches: 3 Dest Hold Misma	ROBERT F. Steven R. Steven R. Steven R. Provided R. Steven R. ROBER: US/10/715,667 ROBER: US/09/972,708 ROBER: US/
	961 341 1021 361 1081 381 1141 401 1261 441 1321 441 1381 1441 1381 1441 1561 1561 1621 581 1741	241 CysGlyLev

Qy 43 Cy8ValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62	Qy 3 LeuSerProGlnProSerCy8ValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22	Pred. No.:	iens (2366)	PRIOR APPLICATION NUMBER: US 60/214,955 PRIOR FILING DATE: 2000-066-29 PRIOR APPLICATION NUMBER: US 60/267,963 PRIOR FILING DATE: 2001-08-02 NUMBER OF SEQ ID NOS: 93 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 2402	; APPLICANT: Kuijper, Joseph L. ; APPLICANT: Maurer, Mark F. ; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 ; FILE REFERENCE: 00-42 ; CURRENT APPLICATION NUMBER: US/09/892,949 ; CURRENT FILING DATE: 2001-06-26 ; PRIOR APPLICATION NUMBER: US 60/214,282 ; PRIOR FILING DATE: 2000-06-26	US-09-892-949-1 ; Sequence I, Application US/09892949 ; Publication No. US20030096339A1 ; GENERAL INFORMATION: ; APPLICANT: Sprecher, Cindy A. ; APPLICANT: Presnell, Scott R. ; APPLICANT: Geo, Zeren ; APPLICANT: whitmore, Theodore E.	TIUS
B & B & B &	. Qy Db 49	? B & B &	B & B &	B & B &	D Q D Q	D Q D Q	D Q D Q D Q
403 ProPheTrpCysTyrAsnileSerValTyrProMetLeuHisAspLysValGlyGluPro 422	CTTTCCTGGGAATCTGTGTCTCAGGCCACGAACTGGACGATCCAGAGATAAATTAAAA		TyrTyrProGluSerAsnThrAsnLeuThrGluThrMecAsnThrThrAsnGlnGlnGlnCluck	LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu [GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys [103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122

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APPLICANT: Gao, Zeren
APPLICANT: Gao, Zeren
APPLICANT: Kuijper, Joseph L.
APPLICANT: Kuijper, Joseph L.
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APPLICANT: Grant, Francis J.
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APPLICANT: Presnell, Scott R.
APPLICANT: Hammond, Angela K.
APPLICANT: No. US20030215838Alak, Julia E.
APPLICANT: No. US20030215838Alak, Julia E.
APPLICANT: Dillon, Stacey R.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MUL
FILE REFERRICE: 02-02
CURRENT APPLICATION NUMBER: US 60/435,361
PRIOR APPLICATION NUMBER: US 60/435,361
PRIOR APPLICATION NUMBER: US 60/389,108
PRIOR APPLICATION NUMBER: US 60/389,325
PRIOR APPLICATION NUMBER: US 60/389,325
PRIOR APPLICATION NUMBER: US 60/389,108
PRIOR PILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,108
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 183
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 2402
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-351-157-110
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APPLICANT: Whitmore, Theodore B.
APPLICANT: Multper, Joseph L.
APPLICANT: Malyer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/10/772,531
CURRENT FILING DATE: 2004-02-05
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2402
TYPE: DNA
PROCANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Preentell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E
APPLICANT: Kuijper, Joseph L.
APPLICANT: Maurer, Mark F.
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US-10-772-531-1
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NAME/KEY: CDS
LOCATION: (171)...
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                                                                        HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg
                                                                                                                                                                                                                        ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
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                                              CATATGACATACTGGAGATTAGAGAACATAGCGAAAACTGAACCACCTAAGATTTTCCGT
                                                                                                                                    ATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGAATTAAATCT
                                                                                                                                                            IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer
                                                                                                                                                                                                                                                                                                                                        TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 82
                                                                                                                                                                                                                                                                                                                                                                                                         TGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAAACCAGT
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3465.50
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Matches:
Conservative:
Mismatches:
Indels:
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ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu

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	503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn
9 9	LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer
ύ öö	LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPheSer
462 1517	GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg
4 4	423 TyrserileGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal
	403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro
ωö	LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys
N m	LeuAspValAsmThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr
N S	GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAla
4. 4	LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle
	GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly
0 0	TyrTyrProGluSerasnThrasnLeuThrGluThrMetAsnThrThrasnGlnGlnLeu
282 977	LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsmIleTrp
262 917	LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu
242 857	PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluGlaAlaProCysGly
222 797	GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys
202 737	ACT Thr
182 677	AlaProvalSerSerAspLeuLysTyrThrLeuArgPheArgThrvalAsnSerThrSer
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US-09-972-708-3

US-09-972-708-3

Sequence 3, Application US/09972708

Publication No. US20030059871A1

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Cosman, David J.

APPLICANT: Mosley, Bruce A.

APPLICANT: Bird, Timothy A.

APPLICANT: Wiley, Steven R.

FITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND

FILE REFERENCE: 3160-B

CURRENT APPLICATION NUMBER: US/09/972,708

CURRENT FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 2480

TYPE: DNA

ORGANISM: Homo sapiens

US-09-972-708-3
                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                     IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu
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420 1391	401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly (
400 1331	ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspL 	
380 1271	SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAs 	
360 1211	CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLys 	
340 1151	LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPhe 	
320 1091	GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsn 	
300	IleTzpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnc	
280 971	ArgLeuLeuTzpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 	
260 911	CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal	
240 851	SerLyBPheTrpSerAspTrpSerGlnGluLyBMetGlyMetThrGluGluGluAlaPro	
220 791	LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 	
200 731	ThrsettpmetGluValasnPheAlaLysAsnArgLysAspLysAsnClnThrTyrAsn	
180	GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 	
160 611	PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro	
140 551	LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 	
120 491	IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle	
100 431	CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPheDheLeuDroArg	
80 371	rSerTyrThrG1nTyrThrValLysArgThrTyrAlaPheG1yG1uLysHisAspAsn 	
311	ATTTCCTGTGTCTACTACTATAGGAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAA	

Search completed: February 23, 2005, 20:18:25 Job time: 1102.62 secs

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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_Spool/US10006265/runat_18022005_094658_22193/app_query.fasta_1.2069
-Q=/cgn2 1/USPTO_Spool/US10006265/runat_18022005_094658_22193/app_query.fasta_1.2069
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human10.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER=US10006265_8CGN 1 1 7723 @runat_18022005_094658_22193 -NCFU=6 -ICFU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBIOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -MARN_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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ALIGNMENTS

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AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AK030512 LOCUS DEFINITION TITLE Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P. Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashinco,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Hazada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K. Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) Mus musculus adult male pituitary gland enriched library, clone:5330424C19 produ Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Mus musculus AK030512.1 GI:26326508 HTC; CAP trapper. Mus musculus (house mouse) AK030512 AK030512 11042159 10349636 full insert sequence. 2232 ď Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus mRNA linear HTC 03-APR-2 gland cDNA, RIKEN full-length product:hypothetical protein, Kashiwagi,K., , Watahiki,M., Carninci, P., 03-APR-2004 Itoh, M., genes

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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/db_xref="G1:26326509"
/db_xref="G1:26326509"
/translation="MASTRAGGTNGVRINFKTLSISVFEIVLLTSLVGGGLLLLSIKT
/translation="MASTRAGGTNGVRINFKTLSISVFEIVLLTSLVGGGLLLLSIKT
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SVLTEVASEDSHSTCSRMADEAYSELARQPSSSCQSPGLSPPREDQAQNPYLKNSVTT
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/clone_lib="RIKEN full-length'
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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to $264)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.

Altschul,S.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
                                                                                                                                                                                                  BC071555
BC071555.1
                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                     errors.
                                                                                                                                                                                                                                                                     BC071555
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                                                                                                                                                                                                                                                                                                                                                                                                                        AspLysLeuValIleAspLysLeuValValAsnPheGlyAsnValLeuGlnGluIlePhe 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnAlaGluGlyGlyLysGlyPheSerLysThrValAsnSerSerIleLeuGlnTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TrpLysGluIleProLysSerGluArgLysGlyIleIleCysAsnTyrThrllePheTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATTAAAAGGTCCTGAGACCAGGGTGGAGAACATCGGTCTGAGGACAGCCACGATCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluSerAspAspSerValAsnThrGluAspArgIleLeuLysProCysSerThrProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGGTACCAACGGGGTGAGAATAAACTTCAAGACATTGTCAATCAGTGTGTTTGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyGlyThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSerValPheGluIle
                                                                                                                                                                                                                                                                                                                                      ACAGAGGAAGCTGGAAAGGGTCAGGCGAGCATTTTGGGAGAGAGCGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGACTGGAAACTCTGGGGACACAGAAGACGTGGTCCTAAAACCATGTCCCGTCCCCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGGCCTCAGAAAGCCAAACCGGTTGACTCCCCTGTGTTGTCCTGATGTTCCCAACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrGlyLeuLysLysProAsnLysLeuThrHisLeuCysTrpProThrValProAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGAGTCTCTGACACGAAGGACCTCTTATACTGTTTGGGTCATGGCCAGCACCAGAGCT
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67.74%
20.85%
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Matches:
Conservative:
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Indels:
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                US-10-006-265-17 (1-662) x BC071555 (1-5264)
                                                                                                                                                                                                                                                                                                                                                                        Query Match:
DB:
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Best Local Similarity:
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                                     581
                                                                                                                                                                    521
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2861014
This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Contact: (Schomutz, J., Grimwood, J., Rodriquez, A., and Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COntact: "To contact of the Contact 
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Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg, R.
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                                  TGGGATGGTGGAAGGGAAACACACTTGGAGACAAACTTCACTTTAAAATCTGAATGGGCA
                                                                                                   TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys------Arg
                                                                                                                                                                    CCAGAAAAACCTAAAAATTTGAGTTGCATTGTGAACGAGGGGAAGAAAATGAGGTGTGAG
                                                                                                                                                                                                                 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:4374041"
/tissue type="Testis"
/clone_Tib="NJH_MGC_97"
/lab_host="DH10B"
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661.00
46.26%
28.55%
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                                                                    GCAGAGAGCAAATGCTATTTGATAACAGTTACTCCAGTATATGCTGATGGACCAGGAAGC 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
                                                                                                                                                                                                ATCACAGACTGGCAACAAGAAGATGGTACCGTGCATCGCACCTATTTAAGAGGGAACTTA 160:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAATGGATCTTAAAGCATTCCCCCAAAGATAACATGCTTTGGGTGGAATGGACTACTCCA 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAAATCAGATGCAGCTGTTTTAACTATCCCTGCCTGTGACTTTCAAGCTACTCACCCT 1423
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                                                                                                                           LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
                                                                                                                                                                                                                                                             ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
                                                                                                                                                                                                                                                                                                                               AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCGTGTGGAAGACATTGCCTCCTTTTGAAGCCAATGGAAAAAATCTTGGATTATGAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg
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                                                                                                                                           Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma, Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zha
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AY310138.1 GI:32264598
                                            Unpublished 2 (bases 1
                                                                   Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H., Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.Liver regeneration after PH
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Direct Submission
Submitted (29-MAY-2003) Henan Bioengineering Key Lab, Henan Normal
University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
China
Location/Qualifiers
1. .3055
Accation/Qualifiers
//mol_type="mank"
//strain="Sprayue-Dawley"
//strain="Sprayue-Dawley"
//strain="Sprayue-Dawley"
//strain="Sprayue-Dawley"
//strain="Sprayue-Dawley"
//strain="Sprayue-Dawley"
//obc="liver regeneration related protein LRRG089"
//codon_start="
//protein_id="AaP78746.1"
//protein_i
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Pred. No.:

6.79e-59

Length:
3055
Score:
657.00

Matches:
18
Percent Similarity:
45.26\$

Best Local Similarity:
28.75\$

Mismatches:
280
Query Match:
18.62\$

Gaps:
78

DB:

US-10-006-265-17 (1-662) x AY310138 (1-3055)

TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLysArgThrTyrAla ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54 GTGAAACCCAGCCCACCTCATAATTTGTCAGTGACCAACTCAGAAGAATTATCCAGTATA AlaGluAsnGlyAspGlyVallleLysSerHisMetThrTyrTrpArgLeuGluAsnIle CysSerPhe---PheLeuProArgIleThrIleProAspAsnTyrThrIleGluValGlu 112 PheGlyGluLysHisAspAsnCysThrThrAsnSerSerThrSerGluAsnArgAlaSer CCAGATATACCTACAAATTTGAGTTGCATTGTGAATGAGGGGAAGAACATGCTGTGTCAG TTAAAACTAGCATGGGTCAATTCAGGTTTGGACAGTATTTTAAGG----CTGAAGTCGGAC IleGlnIleGluTrpIleLysProGluLeuAlaProValSerSerAspLeuLysTyrThr AlaLysThrGluProProLysIlePheArgValLysProValLeuGlyIleLysArgMet GCCGAGAATGCCCCTTGGGAATGTCTCCTCAGAGCCTATCAATTTTGACCCCCGTGGATAAA TGCATGATGGGCTATACCCCCATCTATTTTGTC----AACATCGAGGTCTGGGTGGAG ---ACAGAGAAGTTTCCTGATTGTCGAACAAAGCATGGCACGAGC----TGGGACCCAGGAAGGGACATACCTTGAAACAAACTACACTTTGAAGTCAGAGTGGGCA -----TCC 640 152 580 481 700 526 93 757 73

	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	RESULT 4 BB617934 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	Оу 6 Db 21	Qy 63 Db 209	Qy 61 Db 207	Qy 59 Db 201	Оу 5 Db 19	Qy 56 Db 191	1		Qy 5
The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res.	H., Kouda,M., Koya,S., Matsuyama,T., Miyaza,Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sasaki,D., Shibata,K., Shinagawa,A., Shi,Y., Suzuki,H., Tagami,M., Tagawa,A., Takah,Y., Tanaka,T., Toya,T., Muramatsu,M. and House ESTs (Arakawa,T., et al. 2001) ished (2001) t: Yoshihide Hayashizaki t: Yoshihide Hayashizaki t: Yoshihide Hayashizaki t: Yoshihide Hayashizaki t: Genter(GSC). Yokohama Institute	Mammalia, Butheria, Rodentia, Scientagnathi, Muridae, Murinae, Mus. 1 (bases 1 to 663) 1 (bases 1 to 663) 1 Arakawa,T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki,T., Hara,A. Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,	663 bp mRNA linear EST 31- IKEN full-length enriched, adult male pituitary g DNA clone 5330424C19 5', mRNA sequence. GI:15396442 us (house mouse)	48 GluLysAsnGlyThrArgIleLeuSerSerCysProThrSer 661	30 GlnGluIlePheThrAspGluAlaArgThrGlyGlnGluAsnAsnLeuGlyGly 647	10 SerThrProSerAspLysLeuVallleAspLysLeuValValAsnPheGlyAsnValLeu 629	91 AsnieulysGluSerAspAspSerValasnThrGluAspArgIleieulysProCys 609 	80 ThrTrp	60 AsnLysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAla 579	53 AACTCTTGGCCTACAGCAGACGCATCATCATTTGATGACTGCTACCAAATTAAAAAA	LeuThrValAlaTyrGlyLeuLysLysPro 559	530 ValPheGluIleIleLeuIleThrSerLeuIleGlyGlyGlyLeuLeuIleLeuIleIle 549

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Percent Similarity:
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514 GlyGlyThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSerValPheGluIle 533
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci, Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                              GlnAlaGluGlyGlyLysGlyPheSerLysThrValAsnSerSerIleLeuGlnTyrGly 493
                                            CTGGAGTCTCTGACACGAAGGACCTCTTATACTGTTTGGGTCATGGCCAGCACCAGAGCT
                                                                                 LeuGluSerLeuLysArgLysThrSerTyrIleValGlnValMetAlaSerThrSerAla
                                                                                                                                                                                                                        TGGAAGGAGATTCCTAAGAGTGCTAGGAATGGATTTATCAACAATTACACTGTATTTTAC
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/dev_stage="adult"
/lab_host="DH10B"
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs A Comprehensive Collection of Chicken CDNAs Corr. Biol. 12 (22), 1965-1969 (2002)
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Department of Biomolecular Sciences
University of Manchester Institute of Science
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Fax: 01612360409
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              /clone lib="CSEQRBN14"
ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996: 791, except that a significantly longer
reannealing hybridization was used."
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/lab_host="DH10B"
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                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognat.
1 (bases 1 to 637)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched submicrogram amounts of total RNAs by a
Laboratory of Genetics
National Institutes of Health
National Drive, Suite 4000, Baltimore, MD 21224-6820, t
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0932 row: D column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF174021
637 bp mRNA linear EST 25-JUL-2003
B0932D09-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
musculus cDNA clone NIA:B0932D09 IMAGE:30475340 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                       CF174021
CF174021.1 GI:33283570
                                                                                                            Contact: Dawood
                                                                                                                                                                        Genome Res. 11
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
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47.47%
13.42%
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                                                                                                            B. Dudekula
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Rodentia;
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                                                                                                                                                                                                               enriched cDNA libraries from
NAs by a universal PCR amplification
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                       CCTCTGGGTGTGAACGCTGGAATAATGTGGACCTTGGCACTGTGGGCATTCTCTTTCCTC 178
    GACATCTGCAGTGTTGAAGTACAAGCTCAAAATGGAGATGGTAAAGTTAAATCTGACATC
                          AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHisMet 124
                                                                                                                         ThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIle-----Pro
                                                                                                                                                                          ATTGTGACTTTGACTTACTCCTATGGAAAA-----
                                                                                                                                                                                                             ThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThrThrAsnSerSer 86
                                                                                                                                                                                                                                                                                    TyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGlnTyr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSerLeu 26
                                                                                                                                                                                                                                                            TTCGACAGAAATCTGACTTGCACTTGGAGACCAGAGAAAGGAAACCAATGATACCAGCTAT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall; Site_2: NotI; Mouse cDNA project by the Labbratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA) This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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| ab_host="DH10B"
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'db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain="C57BL/6J"
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63.59%
52.17%
13.28%
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Conservative:
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ORGANISM
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VERSION
KEYWORDS
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotati of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2804)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci, Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hirozane,T., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashic, T., Hoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                      The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTC; CAP trapper.
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                                                                                                                                                                                    The FANTOM Consortium and the RIKEN
                                                                                                                                                                                                                            Nature 409,
                                                                                                                                                                                                                                                Functional
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                                                              Carninci, P.,
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                         631 CAGTGGGAGCCAGGTCCTGAGACCCACCTGCCCACCAGCTTCATCCTAAAG-----
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Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinayawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M., and Hayashizaki,Y.
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URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHisMetThrTyr 126
                                                                                                                                                                                                                                                                AlaPheGlyGluLysHisAspAsnCysThrThrAsnSerSerThr------
                                                                                    GCAAAGAAGAAGGCAGAACAACTGCTCCATCCCCGAAAAAAACTTGCTCCTGTACCAGTAT 798
                                                                                                                                          ---SerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIleProAspAsn
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/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="colony stimulating factor 3 receptor (granulocyte) (MGD MGI:1339755, GB NM_007782, evidence: BLASTN, 99%,
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/db_xref="taxon:10090"
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42.11%
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| mouse cDN?
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437 GlyProGluThrLysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGlu 456	1558 GAAGCCCCAGCCTTCTGCCTCAGGGCTATCTCATTGAGTGGGAAATGAGTTCTCCCAGC 1617 392 ThrAsn	AlaIleGlnGluLy8SerPheGlnCy8IleGluValMetGlnAlaCy8ValAlaGluAsp	275LysThrLeuGlyTyrAsnIleTrpTyrTyrProGluSerAsnThrAsnLeuThr 292 ::: ::: ::: ::: ::: ::: ::: :::	220 GluSerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 237	160 ProGluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsn 179	799 ATGGCCATCTGGGTGCAAGCAGAGAATATGCTAGGGTCCAGCGAGTCCCCAAAGCTGTGC 858 127 TrpArgLeuGluAsnileAlaLysThrGluProProLysIlePheArgValLys 144 1859 CTCGACCCCATGGATGTTGTGAAATTTGGAGCTCCCATGCTGCAGGCCCTGGACATTGGC 918 145 ProValLeu
Alignment Scores: 5.8e-38 Length: 2592 Score: 462.50 Matches: 165	JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers 12592 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1>2592 /gene="CETSTR" /db_yref="HCM4462" ORIGIN	ring nonneutral evolution from human-chimp-trios ce 302 (5652), 1960-1963 (2003) 302 ases 1 to 2592) A.G., Glanowski,S., Nielson,R., Thomas,P., A.G., Glanowski,S., Nielson,R., Thomas,P., E., Civello,D.R., Lu,F., I era,S., Wang,G., Zheng,X.H., White,T.J., Sn., M.D. and Cargill,M.	ACCESSION Av412152 VERSION Av412152.1 GI:39768117 ROWN GSS. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) CORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 2592) AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams M.D. and Carrill M.		495 GluSerLeuLyBArgLysThrSerTyrIleValGalaSerThrSerAlaGly ::: ::: :::	457 IleProLysSerGluArgLysGlyIleIleCysAsmTyrThrIlePheTyrGln ::: :::: ::: 1852 GTACCTGAGGCCCCTAGGCTGGGGATGATACCCCTCACCACTACACCATCTTCTGGGCC 475 AlaGluGlyGlyLysGlyPheSerLysThrValAsmSerSerIleLeuGlnTyrGlyLeu

REFERENCE 1 (bases 1 to 2792) AUTHORS Strausberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,	Db 1090 GACAGCGGACGGATCCAAGGTTATGTGGTTTCTTGGAGACCCTCAGGCCAGGCTGGGGCC 1149 Qy 291 LeuThrGluThrMetAsnThrThrAsnGlnGlnLeuGluLeuHisLeuGlyGlyGluSer 310 :::	
	GACAGTGCAGCTGTTCT SThrLeuGlYTYrAsnI	
BC040954 BC040954 BC040954 BC040954 BC040954 BC040954 DEFINITION Homo sapiens colony stimulating factor 3 receptor (granulocyte), mRNA (cDNA clone IMAGE:5588879), containing frame-shift errors. ACCESSION BC040954	Qy 239 AlaProCysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAla 254	
	19 LysGluSerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 23 37 CCCTGCCTGGCCACTGGAGCGACTCGAGCCTGGAGCTGAGAACTACCGAACGG 99	
Qy 542 GIYGLYLeuLeuIleLeuIleIleuenthrValAlaTyrGLYLeuLysLysProAsnLys 561 ::: ::: ::: Db 1903 CTCCTGCTGTTGCTCACCTGCCTTGTGGAACTGCCTGGCTCTGTTGCAGCCCCAACAGG 1962	Qy 200 AsnLeuThrGlyLeuGlnProPheThrGluTyrVallleAlaLeuArgCysAlaVal 218	
522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly	180 SerThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyr 19 	
Qy 502 SerTyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521	168	
Qy 482 SerLysThrValAsmSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501 ::: ::: :::	Qy 157 TrplleLysProGluLeuAlaProValSerSer	
462 ArgLysGlyIleIleCysAsnTyTThrIlepFyrGlnAlaGluGlyGlyLysGlyPhe	137 ProProLysIlePheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGlu 1 :::	
	117 AspGlyVallleLysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGlu 13	
Qy 422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441	nGly 1 TGCG 6	
Lyberorneirpcyslyrashileserallyrromecleumisaspuysvalulysiu :::	Qy 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhe 96	
382 ThrieuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu	64ThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 8	
Qy 369MetileGluTrpPheProAspVaIAspSerGluProThr 381 ::	49 LysasnLeuThr	
Qy 351 GluAspGlnLeuValValLysTrpGlnSerSerAlaLeuAspValAsnThrTrp 368	Oy 29 PheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSerCysValTyrTyrTyrArg 48	
TIEPTOALAILEGINGLULYSSETPHEGINCYSLIEGIUVALMCGINALACYSVALALA !::::! NNNNNNNNNNNNNNNGCCCAGCTCTGACCAGACTCCATGCCATG	Qy 9 CysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSerLeuCysLys 28	
CNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN)6-265-17 (1-662) х АҮ412152 (1-2592)	
Db 1150 ATCCTGCCCCTCTGCAACACACAGAGCTCAGCTGCACCTTCCACCTGCCTTCAGAAGCC 1209 311 PheTrpValSerMetIleSerTyrAsnSerLeuGlyLysSerProValAlaThrLeuArg 330	Percent Similarity: 39.84* Conservative: 82 Best Local Similarity: 26.61* Mismatches: 278 Query Match: 13.11* Indels: 95	

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REMARK
COMMENT
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AUTHORS
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27437046
This clone has the following problem: frame shifted.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-DEC-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contact: amadan@ByStemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anura
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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PheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSerCysValTyrTyrTyrArg 48
                                               TGCCTGAAC-----
                                                                                    CysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSerLeuCysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5588879"
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                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="Ovary, pooled/clone_Tib="NIH_MGC_125"/lab_host="DH10B"
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Genome Res. 11 (9), 1553-1558 (2001) 21429098
                                                                                                Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H. Construction of long-transcript enriched
                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 651)
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National Institute on Aging/National Institutes of Health
National Institute 4000, Baltimore, MD 21224-6820, U
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0973 row: F column: 04
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                       TACATTGTGACTTTGACTTACTCCTATGGAAAA----
                                                                 TyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThrThrAsnSer 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: Sall; Site 2: Notl; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 1: 153-158 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Unfertilized Egg"
/lab_host="DH10B"
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/mol_type="mRNA"
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54 ThrTrpSerProGlyLysGluThrSerTyrThrGlnTyrThrValLysArgThrTyr 72	oAlaLysProG GCCAGCCCCT	006-265-17 (1-662) x AY412154 (1-2535)	ty: 25.33% 11.24%	Length: Matches: Conservative:	/locus_tag="HCM4462"	/mol_type="genomic DNA" /dbl_type="genomic DNA" /db.xref="taxon:10090" <1xef335 <1xef335		This sequence was made by sequencing genomic exons and ordering	Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,	., Gla	gene crios Science 302 (5652), 1960-1963 (2003) 14671302 2 (bases 1 to 2535)	Adams, M.D. and Cargill, M	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, R., Lu, F., Murphy, B., Ferriera. S., Wang, G., Zheno, X.H., White, T.J., Sninekv, J.J.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2535)	E E	.1 GI:	AY412154 2535 bp DNA linear GSS 16-DEC-2003 Mus musculus CSF3R gene, VIRTUAL TRANSCRIPT, partial sequence, Genomic survey sequence.		625 AATCCAATTTGTAATAGAATGTTCCAG 651	144 LysProValLeuGlyIleLysArgMetIleGln 154	565 ATCACATATTGGCATTTAATCTCCATAGCAAAAACCGAACCTATAATTTTAAGTGTG 624	124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143	505 CCAGACATCTGCAGTGTTGAAGTACAAGCTCAAAATGGAGATGGTAAAGTTAAATCTGAC 564	104 ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHis 123	::: ::: ATTATAGTGACAATGCTACAGAGGCTTCATATTTCTTTTCCCCGTTCCTGTGCAATGCCC	86 SerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIle 103
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384 SerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGln 397	ValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThrLeu ::: ::::: cttaacaccaTcTGGGTAGACTGGGAAGCCCCCAGCCTTCTGCCTCAGGGCTATCTCATT	1219 GAACGAAGGIGICCAGCIGIGACCGGACICCAIGCCAIG	MetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAlaLeuAsp	ProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIleGluVal :::	305 HisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGlyLysSer 324	285 ProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeuGluLeu 304	AAGCAGGAC	1021 ACACGIGGIGICAGAAAGAAGCAACIAGAICCAGGGACAGGIG-AGIGIGCAGCIGIICIGG 1079	256	238 GluAlaProCysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAsp 255 ::	220 GIUSETLYSPHETITSSERASDITDSERGINGIULYSMEEGIYMEETHIGIUGIU 237			180 SerThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyr 199	 	160 ProGluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsn 179	145 ProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLys 159	658 CTCGACCCCATGGATGTTGTGAAATTGGAGCCTCCCATGCTGCAGGCCCTGGACATTGGC 717	127 TrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgValLys 144	598 ATGGCCATCTGGGTGCAAGCAGAGAATATGCTAGGGTCCAGCGAGTCCCCAAAGCTGTGC 657	107 TyrThrileGluValGluAlaGluAsnGlyAspGlyVallleLysSerHisMetThrTyr 126	538 GCAAAGAAGAGCAGAACAACTGCTCCATCCCCCGAAAAAAACTTGCTCCTGTACCAGTAT 597	88SerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIleProAspAsn 106	::: 37		430 CAGTGGGAGCCAGGTCCTGAGACCCACCTGCCCACCAGCTTCATCCTAAAG 480

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1 (bases 1 to 1931)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization

Unpublished
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                 CR610771 1931 bp n full-length cDNA clone CSODI054YG09 of Homo sapiens (human) CR610771
                                                                                                                                                                              http://fulllength.invitrogen.com/
Faraday Avenue
                                                                                                                                     Genoscope.
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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SerPheTrpValSerMetIleSerTyrAsnSerLeuGlyLysSer------ProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glu-----LysThrLeuGlyTyrAsnIleTrpTyrTyrProGluSerAsnThrAsn
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                                                                              CTGAAGGAGAAC---ATCAGGCCCTTTCAGCTCTATGAGATCATCGTGACTCCCTTGTAC
                                                                                                                                                         GCGAGCAATAGCAACAAGACCTGGAGGATGGAACAGAATGGGAGAGCCACGGGGTTTCTG
                                                                                                                                                                                                                                                                   LeuAspValAsnThrTrp-----ProAsp
                                                                                                                                                                                                                                                                                                                                                      MetGlnAlaCysValAlaGluAsp-----GlnLeuValValLysTrpGlnSerSerAla
                                                                                                                                                                                                                                                                                                                                                                                              GTCTTCTCAGAAAGCAGAGGCCCAGCTCTGACCAGACTCCAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCATCCTGCCCTCTGCAACACACAGAGCTCAGCTGCACCTTCCACCTGCCTTCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LeuThrGluThrMetAsnThrThrAsnGlnGlnLeuGluLeuHisLeuGlyGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGACAGCGGACGGATCCAAGGTTATGTGGTTTCTTGGAGACCCCTCAGGCCAGGCTGGG
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                                                                                                                 IleGlnGlnAspLysLeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeu
                                                                                                                                                                                              ValAspSerGluProThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCAGGAGGTGGCCCTTGTGGCCTATAACTCAGCCGGGACCTCTCGTCCCACTCCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                               -----AlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIleGluVal
                                                                                                                                                                                                                                                                                                                 ----GCCATGGCCCGAGACCCTCACAGCCTCTGGGTAGGCTGGGAGCCCCCC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO54YG09"
/tissue_type="Placenta Co
/plasmid="pCMVSPORT_6"
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RS Strausberg, L. Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butcerfield, S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1098
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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              113 AlaGluAsnGlyAspGlyValIleLysSerHisMetThrTyrTrpArgLeuGluAsnIle 132
                                                                                                                                                                             733 ---ACAGAGAAGTTTCCTGATTGCCAGTCAAAGCATGGCACT------TCA
                                                                                                                           94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLIA at: http://image.llnl.gov Series: IRAK Plate: 16 Row: k Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6754337
This clone has the following problem: no polyA-tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: BCM-HGSC
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                                                                                                                                                                                                                                PheGlyGluLyaHiaAapAanCyaThrThrAanSerSerThrSerGluAanArgAlaSer 93
                                                                     TGTATGGTCAGCTACATGCCCACCTATTATGTC----AACATTGAAGTCTGGGTGGAA 828
                                                                                                                      CysSerPhe---PheLeuProArgIleThrIleProAspAsnTyrThrIleGluValGlu 112
                                                                                                                                                                                                                                                                                                                                           TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLysArgThrTyrAla 73
                                                                                                                                                                                                                                                                                                                                                                                                        CCAGATAAACCTACAAATTTGACTTGCATTGTGAATGAGGGGAAGAATATGCTGTGCCAG 672
                                                                                                                                                                                                                                                                                             TGGGACCCCGGAAGGGAGACTTACCTTGAAACAAACTACACTTTGAAATCAGAGTGGGCA
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ductal carcinoma. 5 month old virgin mouse."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
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Conservative:
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S.W.,

Loulseged, H., Nanavati,

RESULT 13 BC020454 LOCUS

DEFINITION

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ACCESSION VERSION

KEYWORDS

ORGANISM

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Infiltrating

REFERENCE AUTHORS

TITLE

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KEYWORDS
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                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                             AUTHORS
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1474 ACCATCCCCAGC 1485
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S92 bp mRNA linear K0283D09-5N NIA Mouse Unfertilized Egg cDNA Library musculus cDNA clone NIA:K0283D09 IMAGE:30052652 5', CA561173
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Evammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; N
1 (bases 1 to 592)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A.,
Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNI
                    National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaelgsun.grc.nia.nih.gov Plate: K0283 row: D column: 09
                                                                                                                          Unpublished (2001)
Other_ESTs: K0283D09-3
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                              CA561173.1 GI:25105828
                                                                                                        Laboratory of Genetics
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DB:
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                                                              104
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                 ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHis 123
                                                                                                                                              SerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIle-----
                                                                                                                                                                                                                                                                               TACTTCGACAGAAATCTGACTTGCACTTGGAGACCAGAGAAACCAATGATACCAGC 408
                                                                                                                                                                                                                                                                                                   TyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGln 65
                                                                                                      AATTATAGTGACAATGCTACAGAGGCTTCATATTCTTTTCCCCCGTTCCTGTGCAATGCCC
                                                                                                                                                                                          TACATTGTGACTTGACTTACTCCTATGGAAAA-----AGC
                                                                                                                                                                                                              TyrThrValLy8ArgThrTyrAlaPheGlyGluLy8Hi8AspAsnCy8ThrThrAsnSer 85
                                                                                                                                                                                                                                                                                                                                                                   CTCTGCAAATTCAGCCTGGCAGTCCTGCCGACTAAGCCAGAGAACATTTCCTGCGTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centrioon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Plao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs.

Double-transded cDNAs were synthesized with an Oligo (dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="NIA Mouse Unfertilized Egg cDNA Library
(Long)"
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/lab_host="DH10B"
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Matches:
Conservative:
Mismatches:
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Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Stagg, C.A., Martin, P., Aiba, K., Tanaka, T. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: K0279 row: C column: 07 Seq.primer: M13 Reverse
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Contact: Dawood B. Dudekula
Laboratory of Genetics
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                                                                                                                                                           treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coll host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pSPORT1 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo (dT)
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